wwPDB EM Validation Summary Report ⓘ

Jan 28, 2023 – 08:05 am GMT

PDB ID	:	7OYB
EMDB ID	:	EMD-13112
Title	:	Cryo-EM structure of the 6 hpf zebrafish embryo 80S ribosome
Authors	:	Leesch, F.; Lorenzo-Orts, L.; Grishkovskaya, I.; Kandolf, S.; Belacic, K.; Meinhart, A.; Haselbach, D.; Pauli, A.
Deposited on	:	2021-06-24
Resolution	:	2.40 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

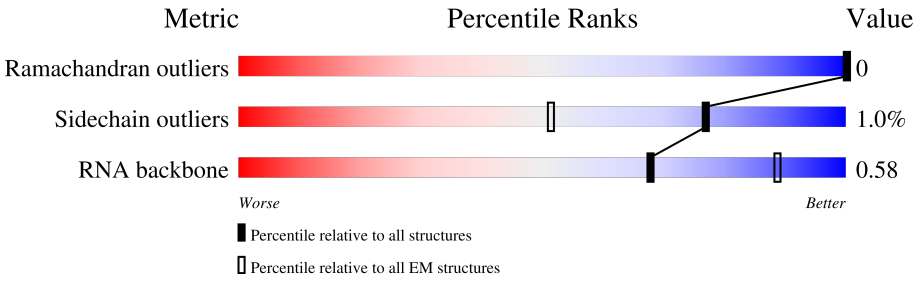
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	22	1939	62% 15% 23%
2	51	4269	63% 14% 24%
3	71	120	95% 5%
4	81	158	83% 12% 5%
5	A1	257	94% 5%
6	A2	308	67% 32%
7	B1	403	98%
8	B2	267	8% 79% 20%

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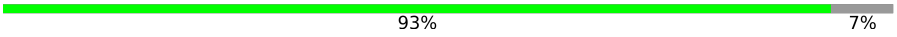
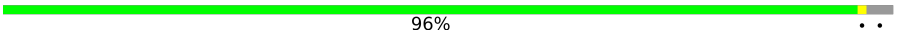
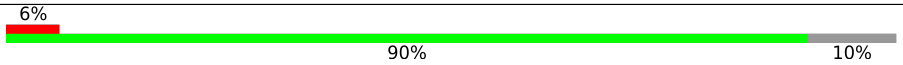
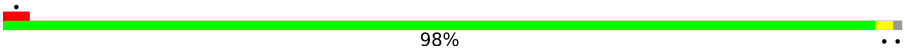
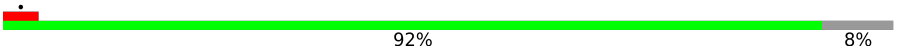
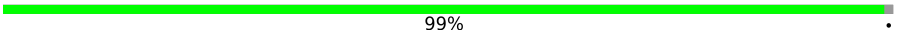
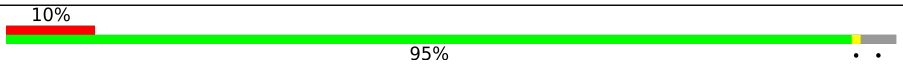
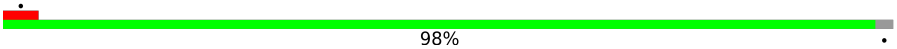
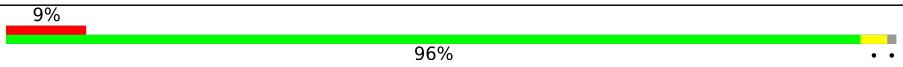
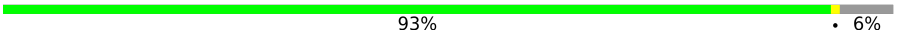
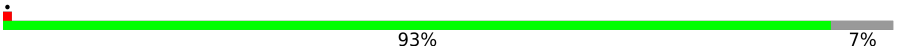
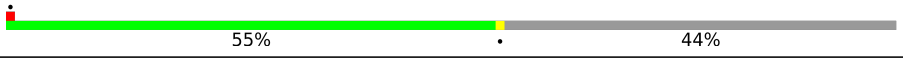
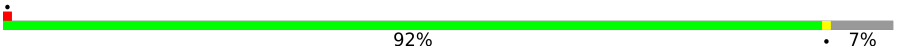
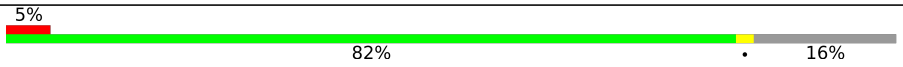
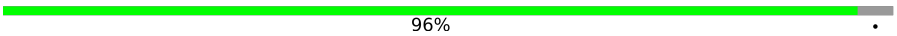
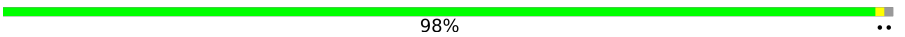
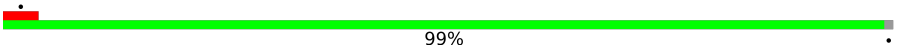
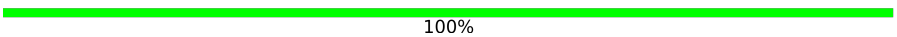
Mol	Chain	Length	Quality of chain
9	C1	375	
10	C2	280	
11	D1	296	
12	D2	245	
13	E1	265	
14	E2	263	
15	F1	246	
16	F2	204	
17	G1	266	
18	G2	249	
19	H1	192	
20	H2	194	
21	I1	215	
22	I2	208	
23	J1	178	
24	J2	194	
25	K2	166	
26	L1	211	
27	L2	159	
28	M1	139	
29	N1	204	
30	N2	151	
31	O1	205	
32	O2	151	
33	P1	184	

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Mol	Chain	Length	Quality of chain
34	P2	145	79% 20%
35	Q1	182	98%
36	Q2	146	90% 8%
37	R1	196	84% 15%
38	R2	134	12% 98%
39	S1	176	99%
40	S2	152	89% 11%
41	T1	160	98%
42	T2	146	93% 6%
43	U1	141	67% 31%
44	U2	119	82% 18%
45	V1	140	92% 8%
46	V2	81	99%
47	W1	157	38% 62%
48	W2	130	98%
49	X1	155	75% 25%
50	X2	143	97%
51	Y1	145	83% 16%
52	Y2	132	5% 93% 6%
53	Z1	136	99%
54	Z2	124	53% 47%
55	a1	148	98%
56	a2	115	84% 15%
57	b1	64	75% 23%
58	b2	84	96%

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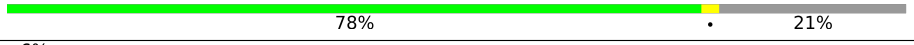
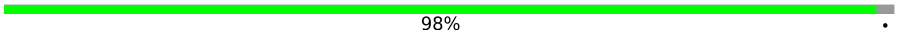
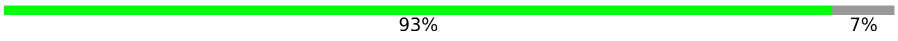
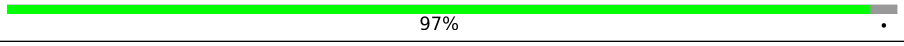
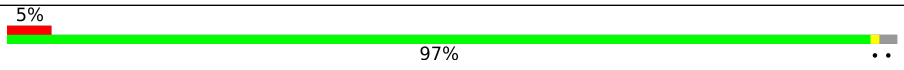
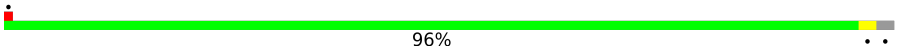
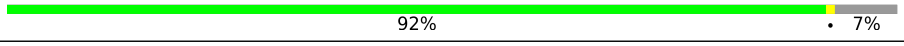
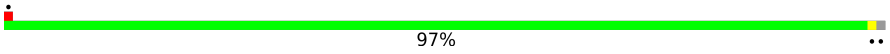
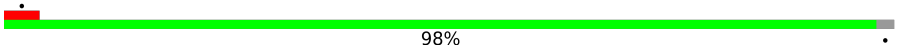
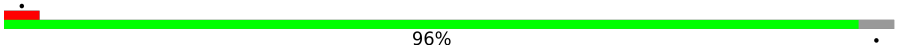
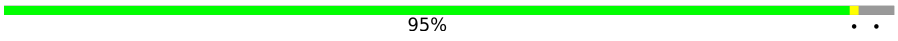
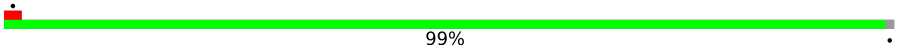
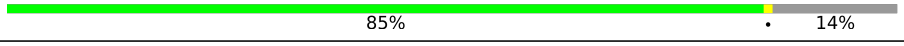
Mol	Chain	Length	Quality of chain
59	c1	117	
60	c2	69	
61	d1	123	
62	d2	56	
63	e1	135	
64	e2	133	
65	f1	110	
66	g1	117	
67	g2	317	
68	h1	123	
69	i1	105	
70	j1	97	
71	k1	70	
72	l1	50	
73	m1	128	
74	n1	25	
75	o1	106	
76	p1	92	
77	r1	138	

2 Entry composition (i)

There are 79 unique types of molecules in this entry. The entry contains 194863 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	22	1502	32102	14330	5809	10462	1501	0	0

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	51	3263	69917	31143	12776	22736	3262	0	0

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	71	120	2563	1145	465	834	119	0	0

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	81	150	3199	1427	574	1048	150	0	0

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A1	245	1879	1181	381	310	7	0	0

- Molecule 6 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A2	210	1665	1061	290	305	9	0	0

- Molecule 7 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B1	394	Total	C	N	O	S	0	0
			3181	2021	600	544	16		

- Molecule 8 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B2	213	Total	C	N	O	S	0	0
			1730	1097	310	309	14		

- Molecule 9 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C1	348	Total	C	N	O	S	0	0
			2774	1741	551	464	18		

- Molecule 10 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C2	213	Total	C	N	O	S	0	0
			1651	1069	283	290	9		

- Molecule 11 is a protein called Ribosomal protein L5b.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D1	288	Total	C	N	O	S	0	0
			2337	1482	429	415	11		

- Molecule 12 is a protein called DNA-(apurinic or apyrimidinic site) lyase.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D2	221	Total	C	N	O	S	0	0
			1713	1091	309	306	7		

- Molecule 13 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E1	206	Total	C	N	O	S	0	0
			1671	1065	327	272	7		

- Molecule 14 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E2	261	Total	C	N	O	S	0	0
			2070	1320	385	357	8		

- Molecule 15 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F1	222	Total	C	N	O	S	0	0
			1811	1160	346	298	7		

- Molecule 16 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	F2	183	Total	C	N	O	S	0	0
			1442	904	268	264	6		

- Molecule 17 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	G1	207	Total	C	N	O	S	0	0
			1683	1076	322	281	4		

- Molecule 18 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G2	230	Total	C	N	O	S	0	0
			1864	1163	375	319	7		

- Molecule 19 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	H1	190	Total	C	N	O	S	0	0
			1505	949	279	271	6		

- Molecule 20 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	H2	186	Total	C	N	O	0	0
			1492	952	276	264		

- Molecule 21 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	I1	211	Total	C	N	O	S	0	0
			1699	1076	329	279	15		

- Molecule 22 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	I2	206	Total	C	N	O	S	0	0
			1666	1047	329	285	5		

- Molecule 23 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	J1	167	Total	C	N	O	S	0	0
			1348	854	254	235	5		

- Molecule 24 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	J2	180	Total	C	N	O	S	0	0
			1492	952	295	243	2		

- Molecule 25 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	K2	93	Total	C	N	O	S	0	0
			769	507	131	127	4		

- Molecule 26 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	L1	197	Total	C	N	O	S	0	0
			1603	1003	335	260	5		

- Molecule 27 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L2	133	Total	C	N	O	S	0	0
			1086	686	211	183	6		

- Molecule 28 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	M1	134	Total	C	N	O	S	0	0
			1094	702	207	180	5		

- Molecule 29 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	N1	202	Total	C	N	O	S	0	0
			1689	1065	352	267	5		

- Molecule 30 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N2	149	Total	C	N	O	S	0	0
			1200	767	230	202	1		

- Molecule 31 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	O1	204	Total	C	N	O	S	0	0
			1662	1073	318	266	5		

- Molecule 32 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	O2	126	Total	C	N	O	S	0	0
			943	579	186	172	6		

- Molecule 33 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	P1	152	Total	C	N	O	S	0	0
			1235	770	243	213	9		

- Molecule 34 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	P2	116	Total	C	N	O	S	0	0
			957	608	177	165	7		

- Molecule 35 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Q1	180	Total	C	N	O	S	0	0
			1459	917	302	236	4		

- Molecule 36 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Q2	134	Total	C	N	O	S	0	0
			1052	671	196	182	3		

- Molecule 37 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	R1	166	Total	C	N	O	S	0	0
			1381	856	300	215	10		

- Molecule 38 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	R2	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 39 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	S1	176	Total	C	N	O	S	0	0
			1457	934	284	230	9		

- Molecule 40 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S2	136	Total	C	N	O	S	0	0
			1129	708	228	192	1		

- Molecule 41 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	T1	157	Total	C	N	O	S	0	0
			1283	816	250	213	4		

- Molecule 42 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	T2	137	Total	C	N	O	S	0	0
			1058	667	202	185	4		

- Molecule 43 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	U1	97	Total	C	N	O	S	0	0
			792	508	138	144	2		

- Molecule 44 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	U2	97	Total	C	N	O	S	0	0
			754	473	139	138	4		

- Molecule 45 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	V1	129	Total	C	N	O	S	0	0
			970	613	182	170	5		

- Molecule 46 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V2	81	Total	C	N	O	S	0	0
			623	384	116	119	4		

- Molecule 47 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W1	60	Total	C	N	O	S	0	0
			503	323	98	80	2		

- Molecule 48 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	W2	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 49 is a protein called Ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	X1	117	Total	C	N	O	S	0	0
			959	614	179	165	1		

- Molecule 50 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	X2	139	Total	C	N	O	S	0	0
			1083	684	215	181	3		

- Molecule 51 is a protein called ATPase H+ transporting V0 subunit e1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Y1	122	Total	C	N	O	S	0	0
			1024	643	209	169	3		

- Molecule 52 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Y2	124	Total	C	N	O	S	0	0
			1011	643	193	170	5		

- Molecule 53 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Z1	135	Total	C	N	O	S	0	0
			1105	714	208	179	4		

- Molecule 54 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	Z2	66	Total	C	N	O	0	0
			529	343	95	91		

- Molecule 55 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	a1	147	Total	C	N	O	S	0	0
			1164	740	233	188	3		

- Molecule 56 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	a2	98	Total	C	N	O	S	0	0
			782	486	161	130	5		

- Molecule 57 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	b1	49	Total	C	N	O	S	0	0
			419	259	92	67	1		

- Molecule 58 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	b2	81	Total	C	N	O	S	0	0
			636	398	120	111	7		

- Molecule 59 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	c1	93	Total	C	N	O	S	0	0
			721	457	127	131	6		

- Molecule 60 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	c2	61	Total	C	N	O	S	0	0
			475	288	94	91	2		

- Molecule 61 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	d1	107	Total	C	N	O	S	0	0
			888	558	172	156	2		

- Molecule 62 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	d2	55	Total	C	N	O	S	0	0
			459	285	94	75	5		

- Molecule 63 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	e1	125	Total	C	N	O	S	0	0
			1030	649	212	163	6		

- Molecule 64 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	e2	50	Total	C	N	O	0	0
			399	244	88	67		

- Molecule 65 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	f1	107	Total	C	N	O	S	0	0
			861	550	171	137	3		

- Molecule 66 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	g1	104	Total	C	N	O	S	0	0
			833	519	172	136	6		

- Molecule 67 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	g2	310	Total	C	N	O	S	0	0
			2394	1507	418	457	12		

- Molecule 68 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	h1	120	Total	C	N	O	S	0	0
			991	627	197	165	2		

- Molecule 69 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	i1	98	Total	C	N	O	S	0	0
			801	502	170	125	4		

- Molecule 70 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	j1	86	Total	C	N	O	S	0	0
			701	430	155	110	6		

- Molecule 71 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	k1	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 72 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	l1	49	Total	C	N	O	S	0	0
			434	275	97	61	1		

- Molecule 73 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	m1	50	Total	C	N	O	S	0	0
			413	256	87	64	6		

- Molecule 74 is a protein called Rpl41.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	n1	24	Total	C	N	O	S	0	0
			231	140	63	26	2		

- Molecule 75 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	o1	102	Total	C	N	O	S	0	0
			840	526	172	136	6		

- Molecule 76 is a protein called Zgc:171772.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	p1	91	Total	C	N	O	S	0	0
			703	444	132	120	7		

- Molecule 77 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	r1	118	Total	C	N	O	S	0	0
			943	589	193	159	2		

- Molecule 78 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
78	51	189	Total	Mg	0
			189	189	
78	71	3	Total	Mg	0
			3	3	
78	81	4	Total	Mg	0
			4	4	
78	A1	2	Total	Mg	0
			2	2	
78	B1	1	Total	Mg	0
			1	1	
78	V1	1	Total	Mg	0
			1	1	
78	b1	1	Total	Mg	0
			1	1	
78	e1	1	Total	Mg	0
			1	1	
78	m1	1	Total	Mg	0
			1	1	

- Molecule 79 is ZINC ION (three-letter code: ZN) (formula: Zn).

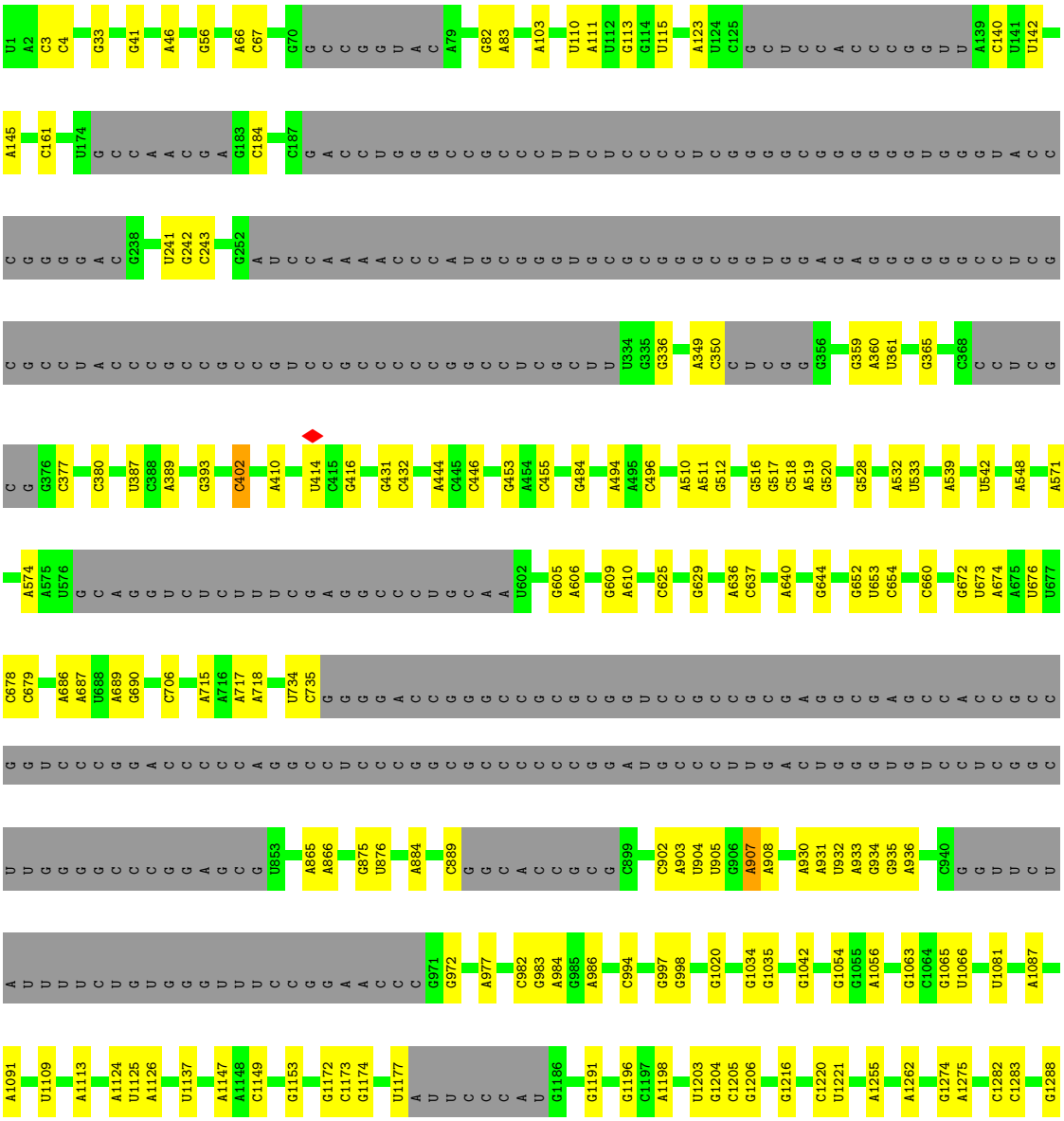
Mol	Chain	Residues	Atoms		AltConf
79	a2	1	Total	Zn	0
			1	1	
79	d2	1	Total	Zn	0
			1	1	
79	g1	1	Total	Zn	0
			1	1	
79	j1	1	Total	Zn	0
			1	1	
79	m1	1	Total	Zn	0
			1	1	
79	o1	1	Total	Zn	0
			1	1	
79	p1	1	Total	Zn	0
			1	1	

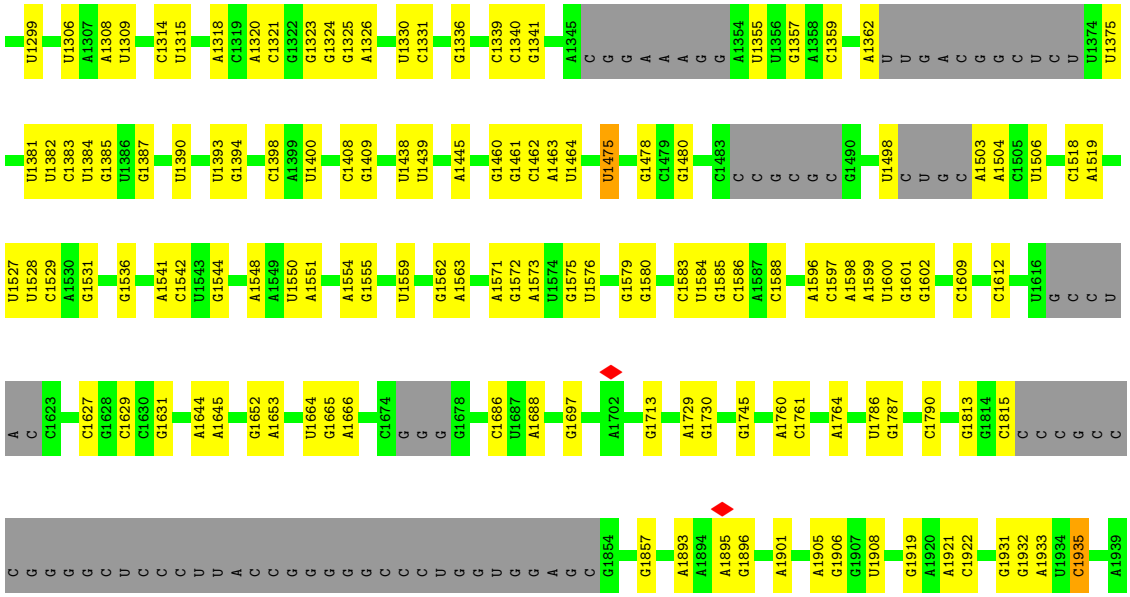
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 18S rRNA

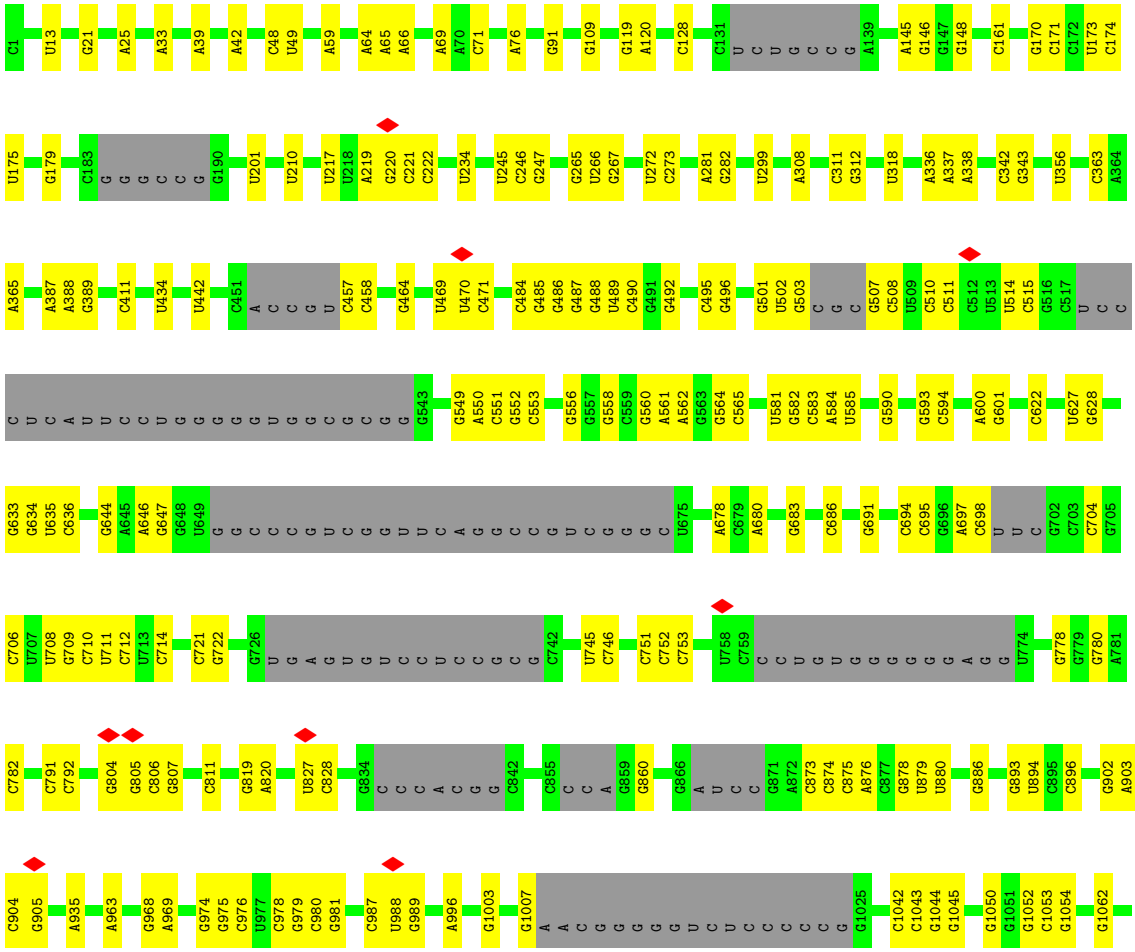
Chain 22:

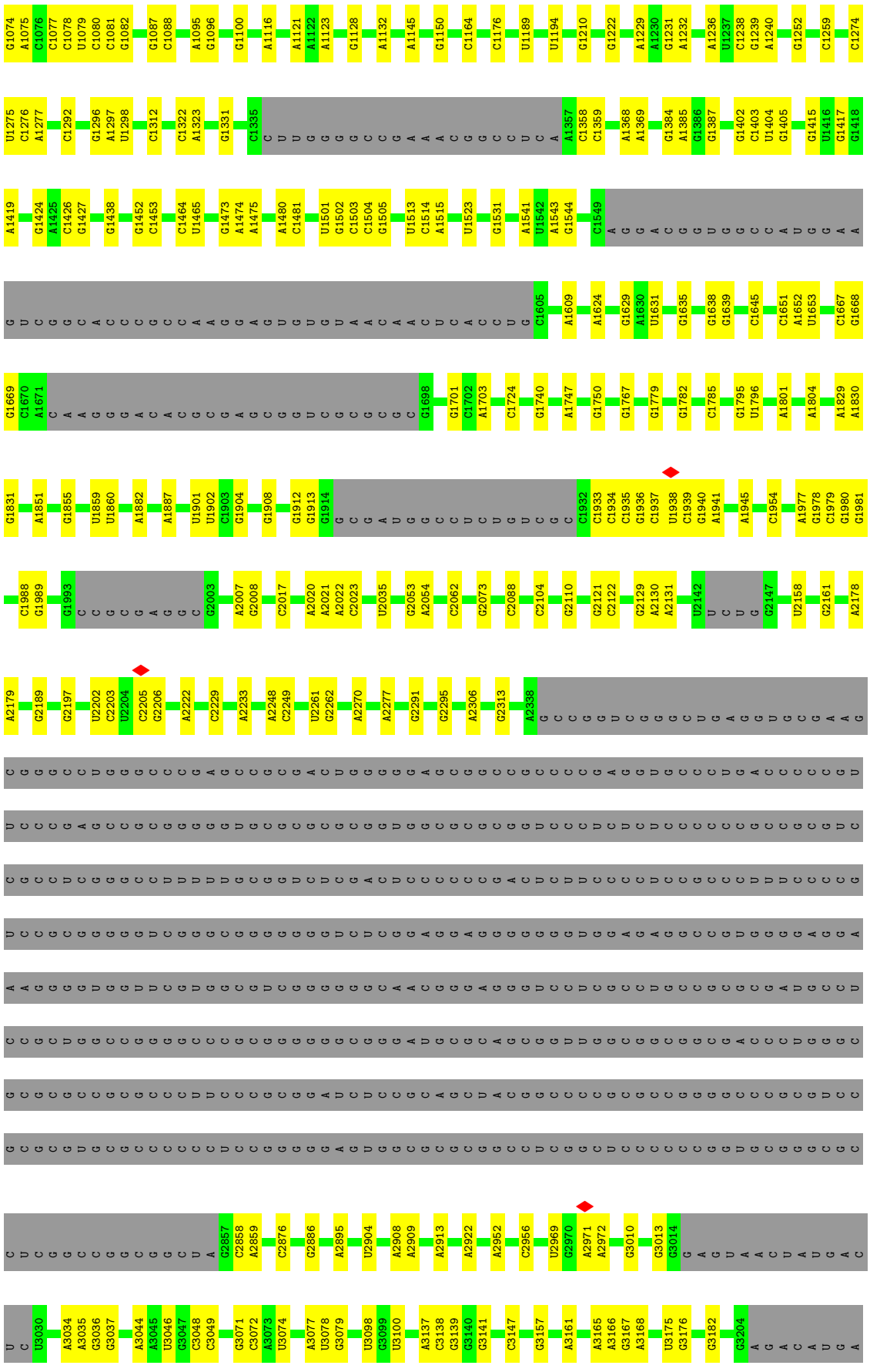


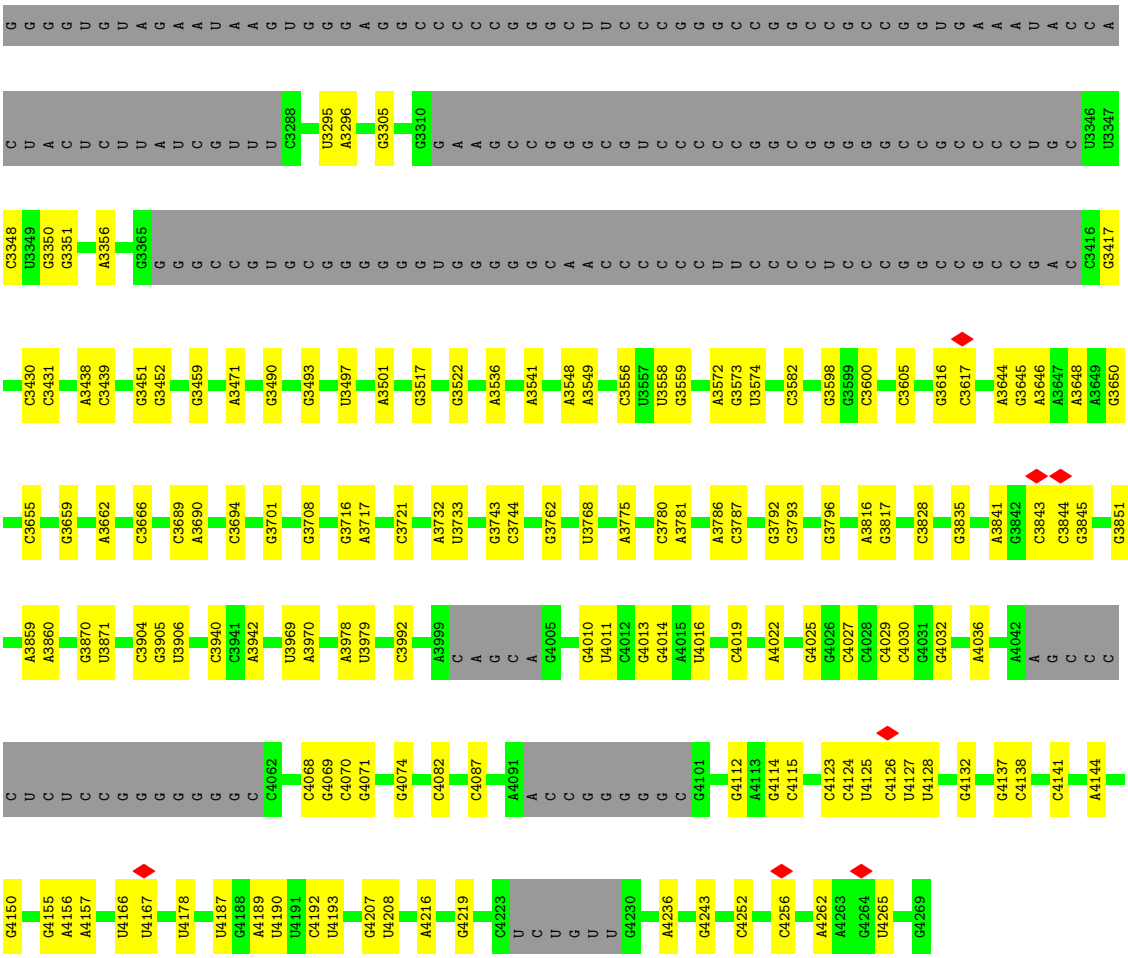


• Molecule 2: 28S rRNA

Chain 51:

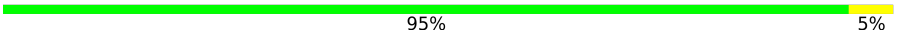


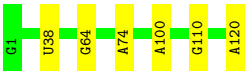




• Molecule 3: 5S rRNA

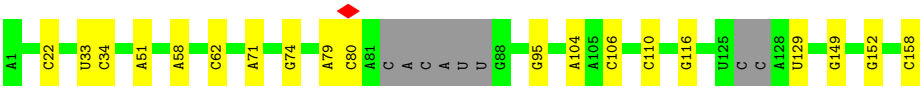
Chain 71:





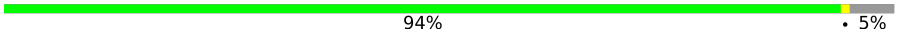
• Molecule 4: 5.8S rRNA

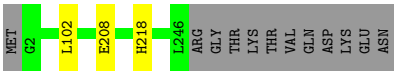
Chain 81:



• Molecule 5: 60S ribosomal protein L8

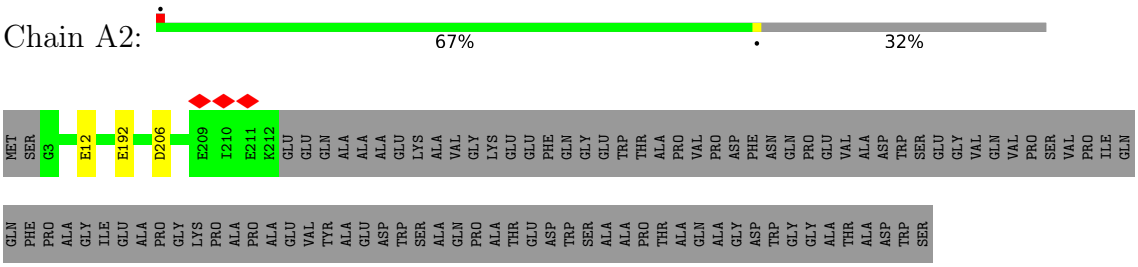
Chain A1:





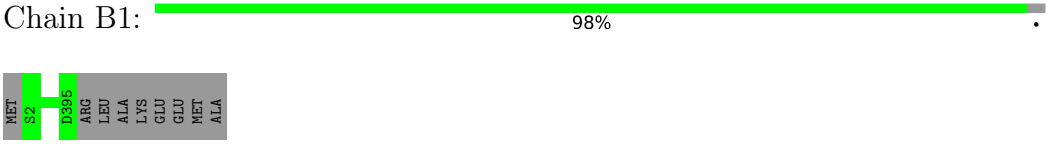
• Molecule 6: 40S ribosomal protein SA

Chain A2:



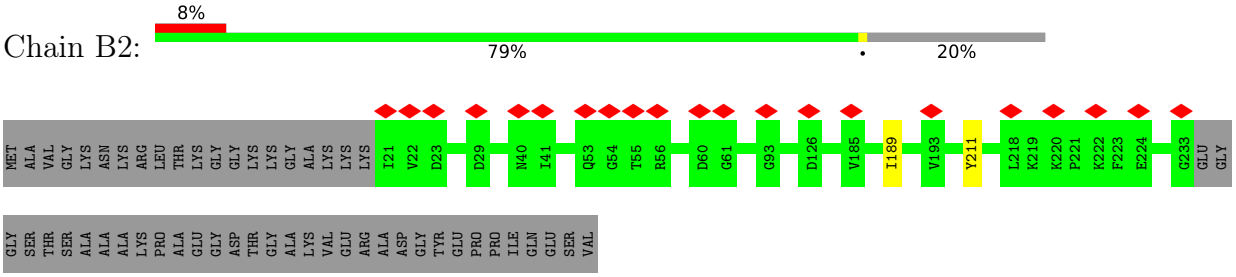
• Molecule 7: Ribosomal protein L3

Chain B1:



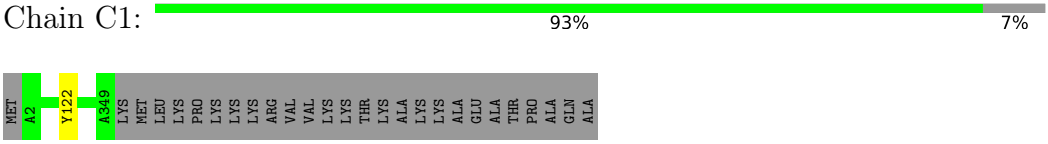
• Molecule 8: 40S ribosomal protein S3a

Chain B2:



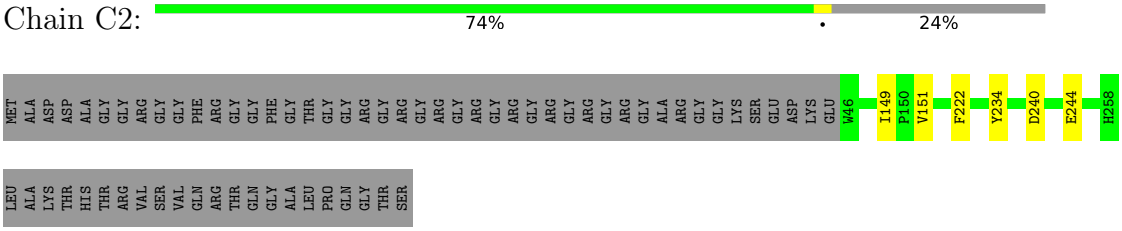
• Molecule 9: Ribosomal protein L4

Chain C1:



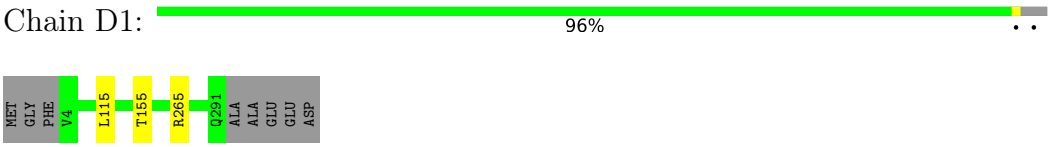
• Molecule 10: 40S ribosomal protein S2

Chain C2:



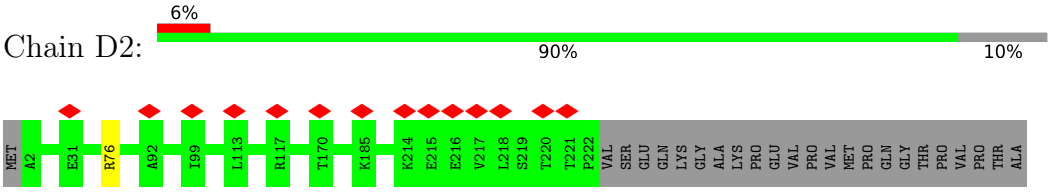
• Molecule 11: Ribosomal protein L5b

Chain D1:



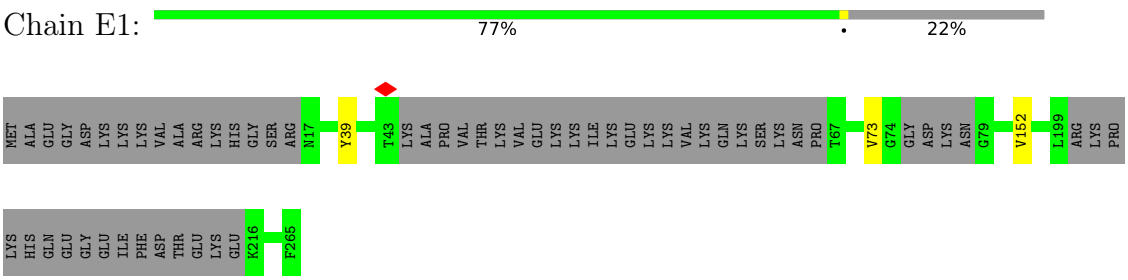
• Molecule 12: DNA-(apurinic or apyrimidinic site) lyase

Chain D2:



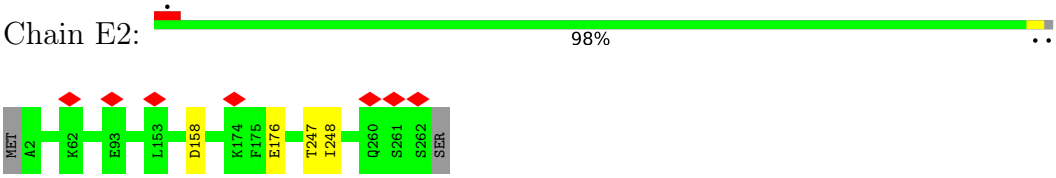
• Molecule 13: 60S ribosomal protein L6

Chain E1:



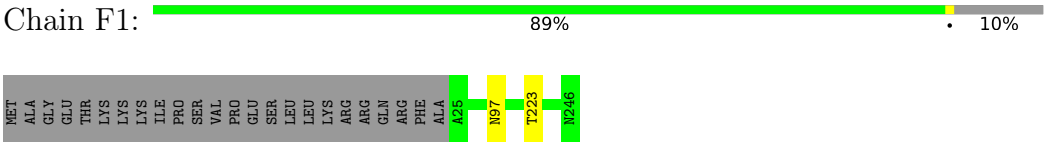
• Molecule 14: 40S ribosomal protein S4, X isoform

Chain E2:



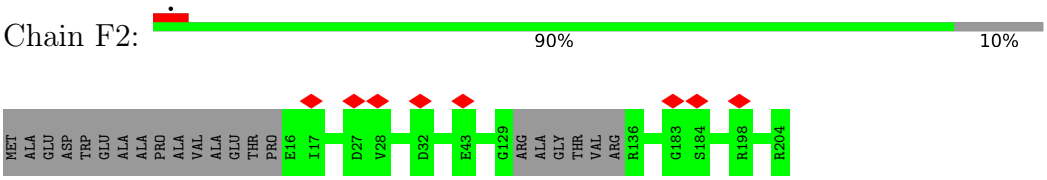
• Molecule 15: Ribosomal protein L7

Chain F1:



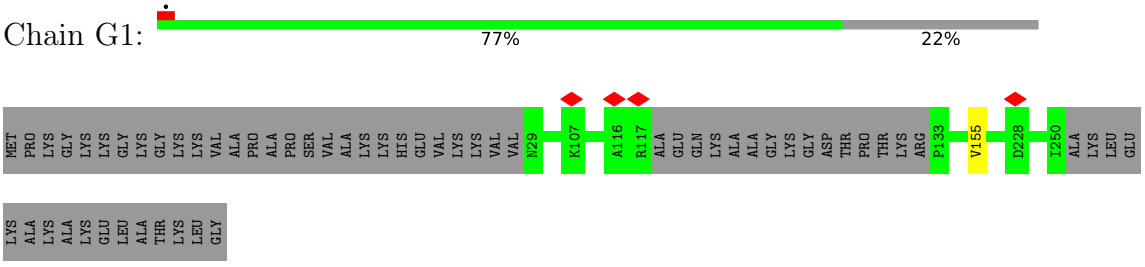
• Molecule 16: Ribosomal protein S5

Chain F2:



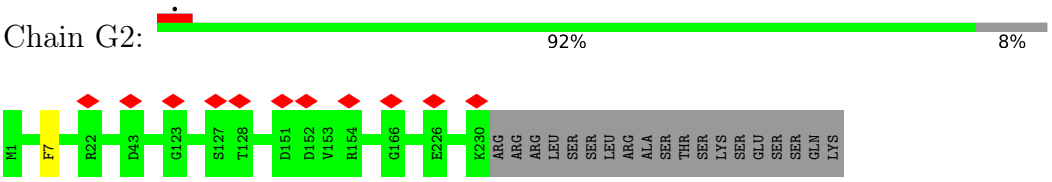
• Molecule 17: 60S ribosomal protein L7a

Chain G1:



• Molecule 18: 40S ribosomal protein S6

Chain G2:

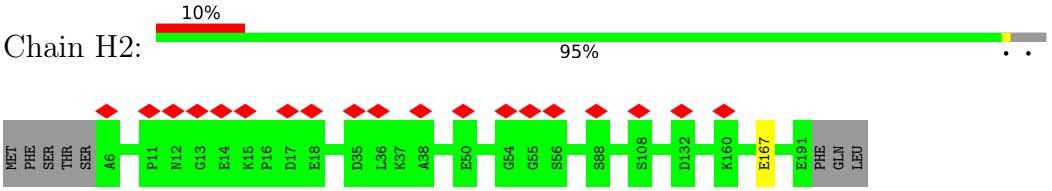


• Molecule 19: 60S ribosomal protein L9

Chain H1:

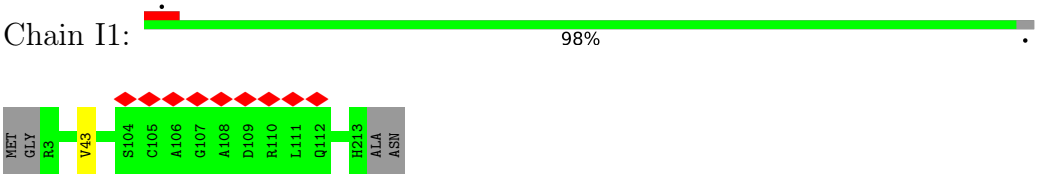
• Molecule 20: 40S ribosomal protein S7

Chain H2:



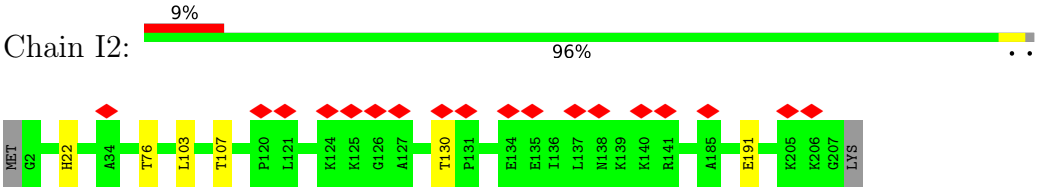
• Molecule 21: 60S ribosomal protein L10

Chain I1:



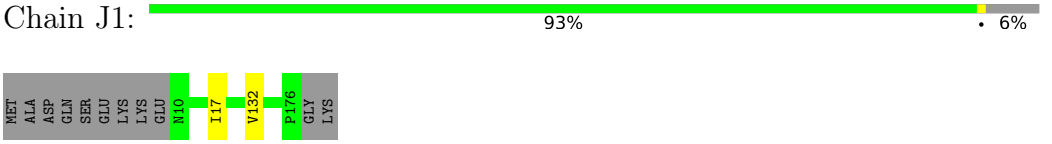
• Molecule 22: 40S ribosomal protein S8

Chain I2:



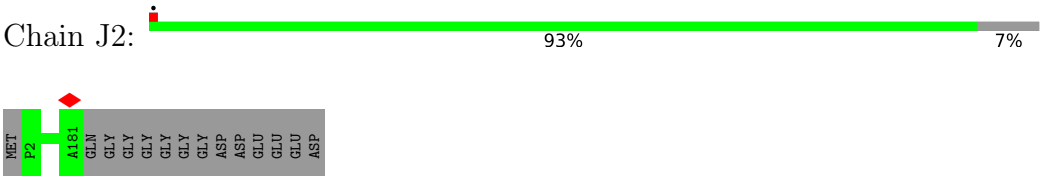
• Molecule 23: 60S ribosomal protein L11

Chain J1:



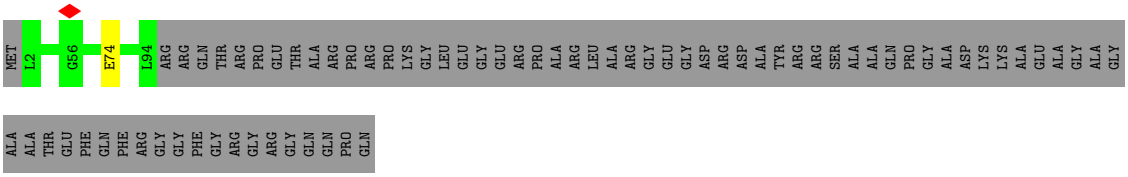
• Molecule 24: 40S ribosomal protein S9

Chain J2:



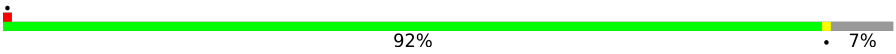
• Molecule 25: Ribosomal protein S10

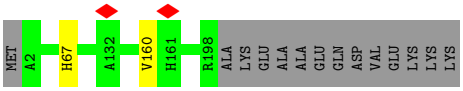
Chain K2:



• Molecule 26: 60S ribosomal protein L13

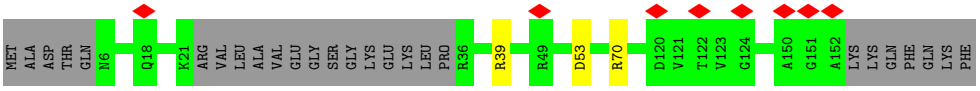
Chain L1:





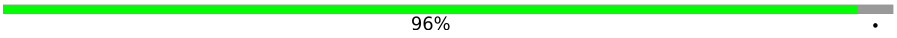
• Molecule 27: 40S ribosomal protein S11

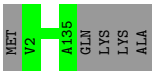
Chain L2:



• Molecule 28: 60S ribosomal protein L14

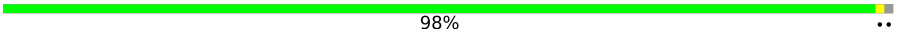
Chain M1:

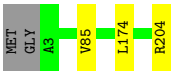




• Molecule 29: Ribosomal protein L15

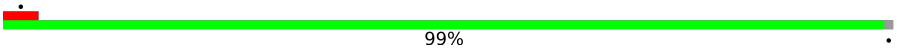
Chain N1:

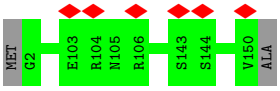




• Molecule 30: 40S ribosomal protein S13

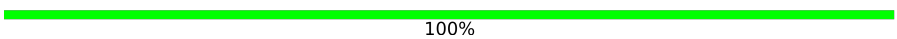
Chain N2:





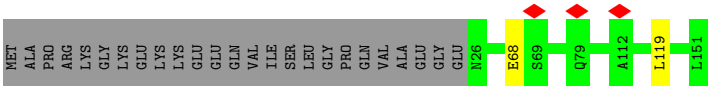
• Molecule 31: 60S ribosomal protein L13a

Chain O1:



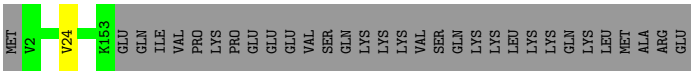
• Molecule 32: Ribosomal protein S14

Chain O2:



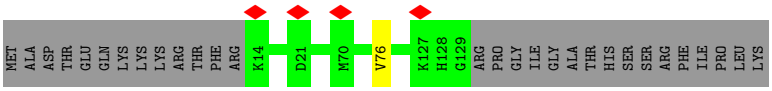
• Molecule 33: 60S ribosomal protein L17

Chain P1:



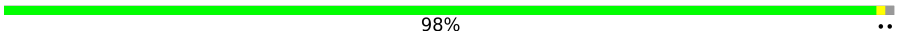
• Molecule 34: 40S ribosomal protein S15

Chain P2:



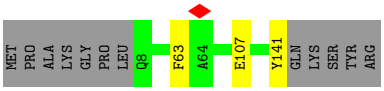
• Molecule 35: Ribosomal protein L18

Chain Q1:



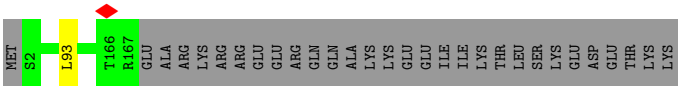
• Molecule 36: Ribosomal protein S16

Chain Q2:



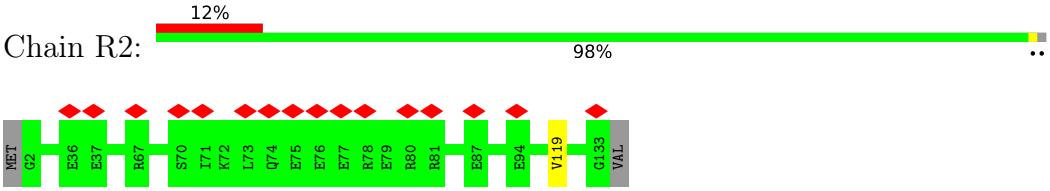
• Molecule 37: 60S ribosomal protein L19

Chain R1:



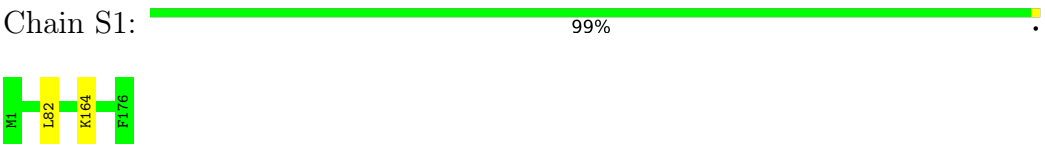
• Molecule 38: 40S ribosomal protein S17

Chain R2:



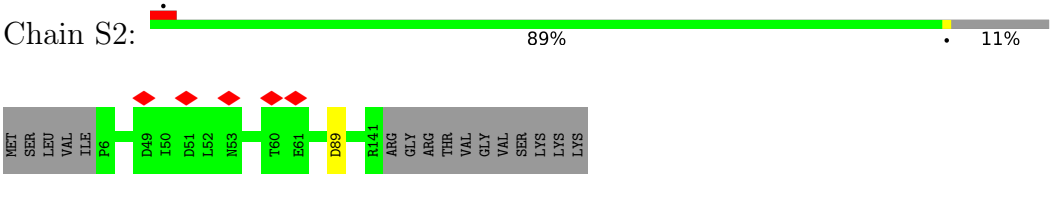
• Molecule 39: 60S ribosomal protein L18a

Chain S1:



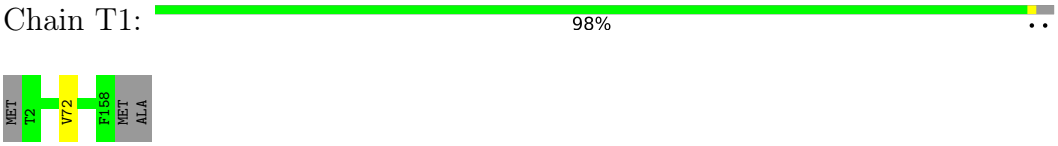
• Molecule 40: 40S ribosomal protein S18

Chain S2:



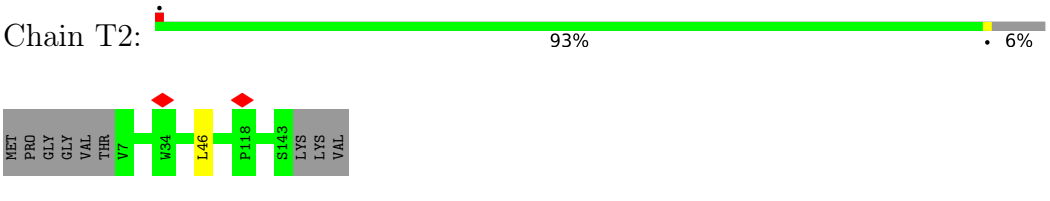
• Molecule 41: 60S ribosomal protein L21

Chain T1:



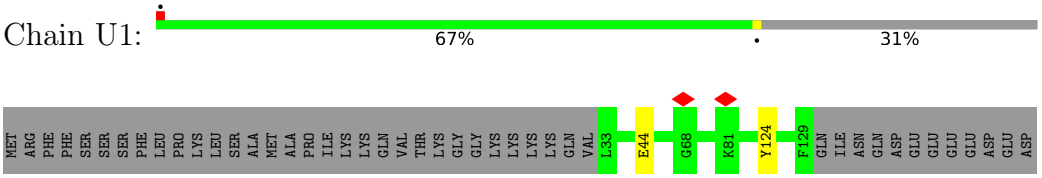
• Molecule 42: 40S ribosomal protein S19

Chain T2:



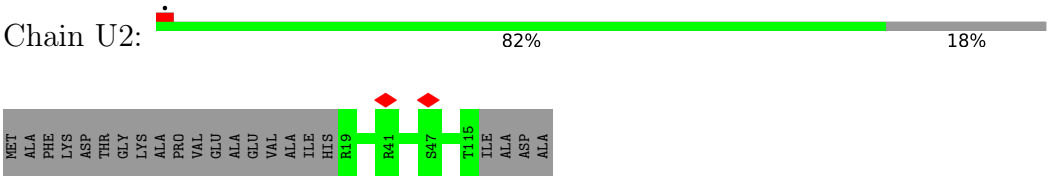
• Molecule 43: Ribosomal protein L22

Chain U1:



• Molecule 44: 40S ribosomal protein S20

Chain U2:

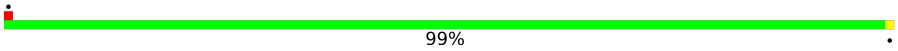


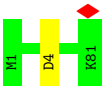
• Molecule 45: 60S ribosomal protein L23

Chain V1:

• Molecule 46: 40S ribosomal protein S21

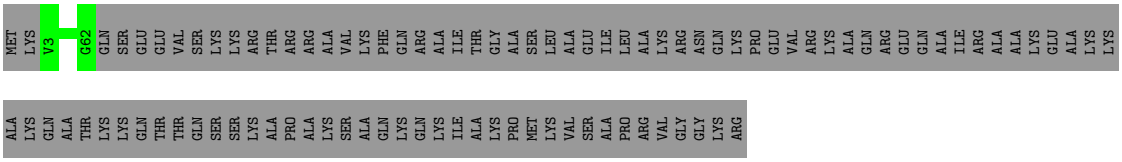
Chain V2:





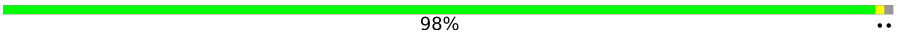
• Molecule 47: 60S ribosomal protein L24

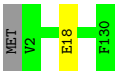
Chain W1:



• Molecule 48: 40S ribosomal protein S15a

Chain W2:



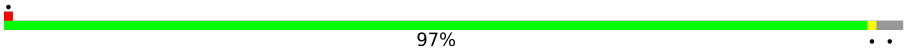


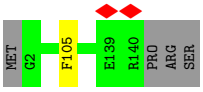
• Molecule 49: Ribosomal protein L23a

Chain X1:

• Molecule 50: 40S ribosomal protein S23

Chain X2:



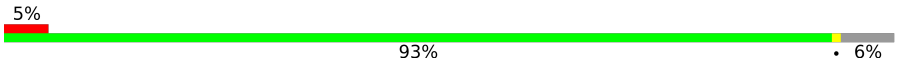


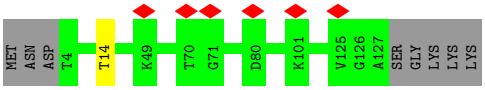
• Molecule 51: ATPase H+ transporting V0 subunit e1

Chain Y1:

• Molecule 52: 40S ribosomal protein S24

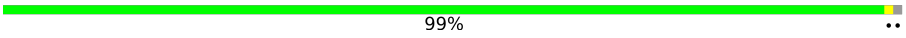
Chain Y2:





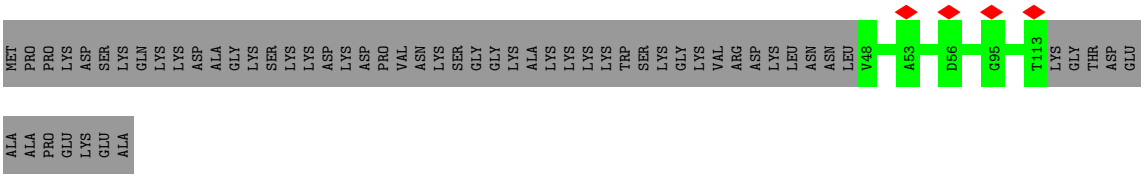
• Molecule 53: 60S ribosomal protein L27

Chain Z1:



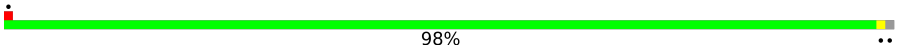
• Molecule 54: 40S ribosomal protein S25

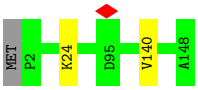
Chain Z2:



• Molecule 55: 60S ribosomal protein L27a

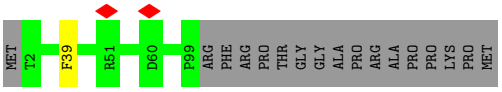
Chain a1:





• Molecule 56: 40S ribosomal protein S26

Chain a2:

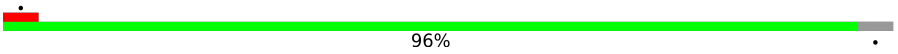


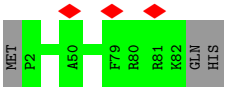
• Molecule 57: 60S ribosomal protein L29

Chain b1:

• Molecule 58: 40S ribosomal protein S27

Chain b2:



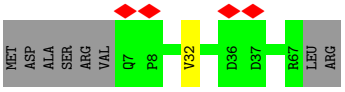


• Molecule 59: 60S ribosomal protein L30

Chain c1:

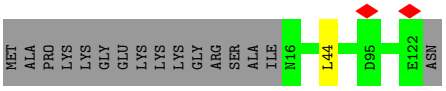
• Molecule 60: 40S ribosomal protein S28

Chain c2:



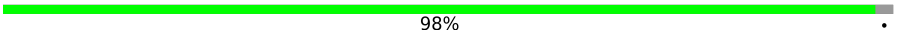
• Molecule 61: 60S ribosomal protein L31

Chain d1:



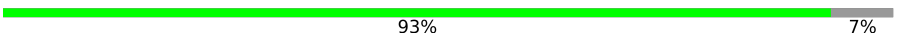
• Molecule 62: 40S ribosomal protein S29

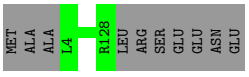
Chain d2:



• Molecule 63: Ribosomal protein L32

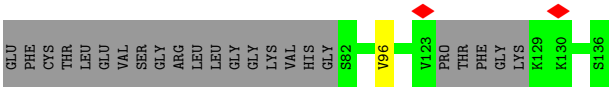
Chain e1:





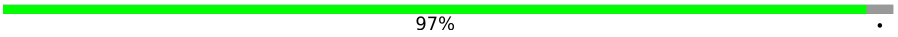
• Molecule 64: 40S ribosomal protein S30

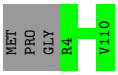
Chain e2:



• Molecule 65: 60S ribosomal protein L35a

Chain f1:



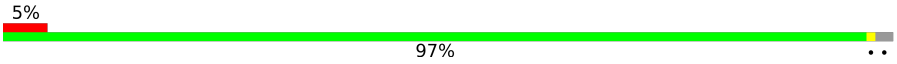


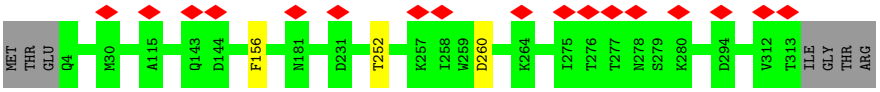
• Molecule 66: 60S ribosomal protein L34

Chain g1:

• Molecule 67: Guanine nucleotide-binding protein subunit beta-2-like 1

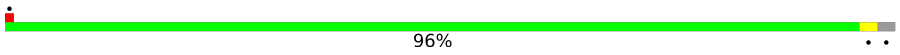
Chain g2:

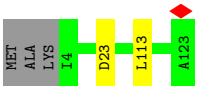




• Molecule 68: 60S ribosomal protein L35

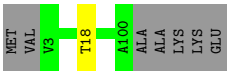
Chain h1:





• Molecule 69: 60S ribosomal protein L36

Chain i1:

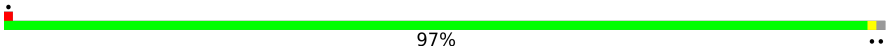


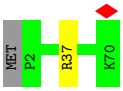
• Molecule 70: Ribosomal protein L37

Chain j1:

• Molecule 71: 60S ribosomal protein L38

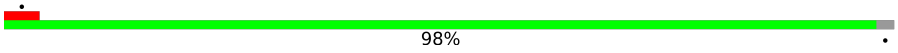
Chain k1:

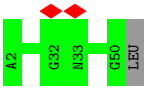




• Molecule 72: Ribosomal protein L39

Chain l1:



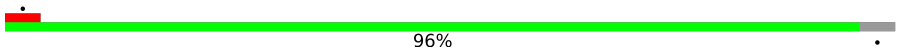


• Molecule 73: 60S ribosomal protein L40

Chain m1:

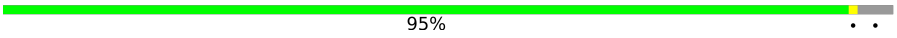
• Molecule 74: Rpl41

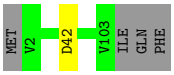
Chain n1:



• Molecule 75: 60S ribosomal protein L36a

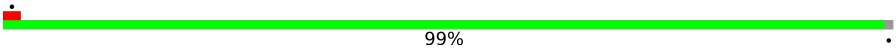
Chain o1:

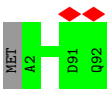




• Molecule 76: Zgc:171772

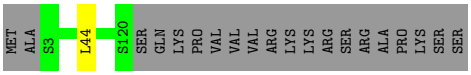
Chain p1:





• Molecule 77: 60S ribosomal protein L28

Chain r1:


MET
ALA
S3
L44
S120
SER
GLN
LYS
PRO
VAL
VAL
VAL
ARG
LYS
LYS
ARG
SER
ARG
ALA
PRO
LYS
SER
SER

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	775288	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	48.3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	10.815	Depositor
Minimum map value	-0.721	Depositor
Average map value	0.068	Depositor
Map value standard deviation	0.247	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	22	0.16	0/35898	0.69	14/55926 (0.0%)
2	51	0.24	0/78190	0.71	8/121918 (0.0%)
3	71	0.22	0/2867	0.66	0/4469
4	81	0.23	0/3573	0.69	0/5563
5	A1	0.25	0/1918	0.42	0/2569
6	A2	0.24	0/1703	0.39	0/2313
7	B1	0.25	0/3251	0.42	0/4351
8	B2	0.23	0/1757	0.41	0/2353
9	C1	0.24	0/2828	0.39	0/3797
10	C2	0.24	0/1687	0.40	0/2281
11	D1	0.25	0/2380	0.39	0/3185
12	D2	0.24	0/1740	0.42	0/2342
13	E1	0.25	0/1697	0.41	0/2264
14	E2	0.24	0/2110	0.42	0/2839
15	F1	0.25	0/1842	0.38	0/2460
16	F2	0.23	0/1462	0.38	0/1966
17	G1	0.24	0/1717	0.39	0/2316
18	G2	0.23	0/1887	0.41	0/2515
19	H1	0.24	0/1523	0.43	0/2048
20	H2	0.23	0/1515	0.41	0/2033
21	I1	0.26	0/1738	0.41	0/2325
22	I2	0.23	0/1695	0.42	0/2267
23	J1	0.24	0/1371	0.41	0/1833
24	J2	0.23	0/1517	0.37	0/2028
25	K2	0.23	0/792	0.39	0/1072
26	L1	0.24	0/1631	0.40	0/2178
27	L2	0.23	0/1105	0.42	0/1479
28	M1	0.25	0/1115	0.37	0/1488
29	N1	0.24	0/1731	0.40	0/2314
30	N2	0.22	0/1223	0.37	0/1644
31	O1	0.24	0/1694	0.38	0/2267
32	O2	0.24	0/955	0.43	0/1279

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
33	P1	0.24	0/1261	0.40	0/1691
34	P2	0.24	0/974	0.39	0/1301
35	Q1	0.24	0/1484	0.41	0/1985
36	Q2	0.23	0/1068	0.40	0/1434
37	R1	0.22	0/1397	0.36	0/1849
38	R2	0.23	0/1082	0.37	0/1452
39	S1	0.26	0/1496	0.40	0/2009
40	S2	0.23	0/1147	0.39	0/1535
41	T1	0.25	0/1312	0.40	0/1756
42	T2	0.23	0/1076	0.37	0/1445
43	U1	0.24	0/806	0.42	0/1081
44	U2	0.23	0/763	0.42	0/1027
45	V1	0.26	0/984	0.43	0/1320
46	V2	0.24	0/629	0.42	0/842
47	W1	0.26	0/516	0.39	0/688
48	W2	0.23	0/1051	0.41	0/1406
49	X1	0.24	0/978	0.40	0/1318
50	X2	0.24	0/1100	0.41	0/1468
51	Y1	0.24	0/1039	0.41	0/1383
52	Y2	0.23	0/1027	0.42	0/1364
53	Z1	0.25	0/1128	0.39	0/1504
54	Z2	0.23	0/536	0.42	0/721
55	a1	0.25	0/1196	0.41	0/1601
56	a2	0.23	0/795	0.41	0/1066
57	b1	0.23	0/429	0.37	0/568
58	b2	0.23	0/649	0.41	0/872
59	c1	0.25	0/731	0.39	0/981
60	c2	0.22	0/477	0.45	0/639
61	d1	0.24	0/903	0.42	0/1217
62	d2	0.23	0/470	0.37	0/624
63	e1	0.24	0/1048	0.40	0/1396
64	e2	0.23	0/401	0.37	0/526
65	f1	0.26	0/880	0.42	0/1175
66	g1	0.24	0/843	0.42	0/1123
67	g2	0.23	0/2451	0.45	0/3343
68	h1	0.23	0/998	0.36	0/1318
69	i1	0.23	0/812	0.36	0/1074
70	j1	0.24	0/715	0.42	0/944
71	k1	0.25	0/575	0.39	0/761
72	l1	0.23	0/444	0.40	0/587
73	m1	0.24	0/419	0.41	0/555
74	n1	0.20	0/232	0.33	0/295
75	o1	0.25	0/853	0.41	0/1125

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
76	p1	0.25	0/713	0.41	0/945
77	r1	0.23	0/956	0.41	0/1279
All	All	0.23	0/208956	0.60	22/306275 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
39	S1	0	1

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	22	676	U	C2-N1-C1'	7.74	126.98	117.70
1	22	676	U	N1-C2-O2	7.31	127.92	122.80
1	22	676	U	N3-C2-O2	-6.83	117.42	122.20
1	22	907	A	P-O3'-C3'	6.36	127.34	119.70
1	22	402	C	C2-N1-C1'	6.16	125.58	118.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
39	S1	164	LYS	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	A1	243/257 (95%)	236 (97%)	7 (3%)	0	100	100
6	A2	208/308 (68%)	204 (98%)	4 (2%)	0	100	100
7	B1	392/403 (97%)	381 (97%)	11 (3%)	0	100	100
8	B2	211/267 (79%)	205 (97%)	6 (3%)	0	100	100
9	C1	346/375 (92%)	336 (97%)	10 (3%)	0	100	100
10	C2	211/280 (75%)	210 (100%)	1 (0%)	0	100	100
11	D1	286/296 (97%)	278 (97%)	8 (3%)	0	100	100
12	D2	219/245 (89%)	208 (95%)	11 (5%)	0	100	100
13	E1	198/265 (75%)	191 (96%)	7 (4%)	0	100	100
14	E2	259/263 (98%)	243 (94%)	16 (6%)	0	100	100
15	F1	220/246 (89%)	215 (98%)	5 (2%)	0	100	100
16	F2	179/204 (88%)	171 (96%)	8 (4%)	0	100	100
17	G1	203/266 (76%)	196 (97%)	7 (3%)	0	100	100
18	G2	228/249 (92%)	220 (96%)	8 (4%)	0	100	100
19	H1	188/192 (98%)	184 (98%)	4 (2%)	0	100	100
20	H2	184/194 (95%)	174 (95%)	10 (5%)	0	100	100
21	I1	209/215 (97%)	201 (96%)	8 (4%)	0	100	100
22	I2	204/208 (98%)	194 (95%)	10 (5%)	0	100	100
23	J1	165/178 (93%)	161 (98%)	4 (2%)	0	100	100
24	J2	178/194 (92%)	177 (99%)	1 (1%)	0	100	100
25	K2	91/166 (55%)	86 (94%)	5 (6%)	0	100	100
26	L1	195/211 (92%)	188 (96%)	7 (4%)	0	100	100
27	L2	129/159 (81%)	123 (95%)	6 (5%)	0	100	100
28	M1	132/139 (95%)	129 (98%)	3 (2%)	0	100	100
29	N1	200/204 (98%)	195 (98%)	5 (2%)	0	100	100
30	N2	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
31	O1	202/205 (98%)	199 (98%)	3 (2%)	0	100	100
32	O2	124/151 (82%)	120 (97%)	4 (3%)	0	100	100
33	P1	150/184 (82%)	143 (95%)	7 (5%)	0	100	100
34	P2	114/145 (79%)	111 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	Q1	178/182 (98%)	171 (96%)	7 (4%)	0	100	100
36	Q2	132/146 (90%)	127 (96%)	5 (4%)	0	100	100
37	R1	164/196 (84%)	163 (99%)	1 (1%)	0	100	100
38	R2	130/134 (97%)	127 (98%)	3 (2%)	0	100	100
39	S1	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
40	S2	134/152 (88%)	127 (95%)	7 (5%)	0	100	100
41	T1	155/160 (97%)	151 (97%)	4 (3%)	0	100	100
42	T2	135/146 (92%)	127 (94%)	8 (6%)	0	100	100
43	U1	95/141 (67%)	90 (95%)	5 (5%)	0	100	100
44	U2	95/119 (80%)	93 (98%)	2 (2%)	0	100	100
45	V1	127/140 (91%)	125 (98%)	2 (2%)	0	100	100
46	V2	79/81 (98%)	78 (99%)	1 (1%)	0	100	100
47	W1	58/157 (37%)	57 (98%)	1 (2%)	0	100	100
48	W2	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
49	X1	115/155 (74%)	112 (97%)	3 (3%)	0	100	100
50	X2	137/143 (96%)	132 (96%)	5 (4%)	0	100	100
51	Y1	120/145 (83%)	116 (97%)	4 (3%)	0	100	100
52	Y2	122/132 (92%)	115 (94%)	7 (6%)	0	100	100
53	Z1	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
54	Z2	64/124 (52%)	61 (95%)	3 (5%)	0	100	100
55	a1	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
56	a2	96/115 (84%)	95 (99%)	1 (1%)	0	100	100
57	b1	47/64 (73%)	44 (94%)	3 (6%)	0	100	100
58	b2	79/84 (94%)	75 (95%)	4 (5%)	0	100	100
59	c1	91/117 (78%)	90 (99%)	1 (1%)	0	100	100
60	c2	59/69 (86%)	58 (98%)	1 (2%)	0	100	100
61	d1	105/123 (85%)	102 (97%)	3 (3%)	0	100	100
62	d2	53/56 (95%)	53 (100%)	0	0	100	100
63	e1	123/135 (91%)	121 (98%)	2 (2%)	0	100	100
64	e2	46/133 (35%)	45 (98%)	1 (2%)	0	100	100
65	f1	105/110 (96%)	104 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	g1	102/117 (87%)	99 (97%)	3 (3%)	0	100	100
67	g2	308/317 (97%)	291 (94%)	17 (6%)	0	100	100
68	h1	118/123 (96%)	114 (97%)	4 (3%)	0	100	100
69	i1	96/105 (91%)	94 (98%)	2 (2%)	0	100	100
70	j1	84/97 (87%)	84 (100%)	0	0	100	100
71	k1	67/70 (96%)	67 (100%)	0	0	100	100
72	l1	47/50 (94%)	46 (98%)	1 (2%)	0	100	100
73	m1	48/128 (38%)	48 (100%)	0	0	100	100
74	n1	22/25 (88%)	22 (100%)	0	0	100	100
75	o1	100/106 (94%)	96 (96%)	4 (4%)	0	100	100
76	p1	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
77	r1	116/138 (84%)	114 (98%)	2 (2%)	0	100	100
All	All	10635/12237 (87%)	10301 (97%)	334 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	A1	189/200 (94%)	186 (98%)	3 (2%)	62	79
6	A2	179/250 (72%)	176 (98%)	3 (2%)	60	78
7	B1	346/353 (98%)	346 (100%)	0	100	100
8	B2	194/231 (84%)	192 (99%)	2 (1%)	76	88
9	C1	291/313 (93%)	290 (100%)	1 (0%)	92	97
10	C2	179/220 (81%)	173 (97%)	6 (3%)	37	56
11	D1	244/249 (98%)	241 (99%)	3 (1%)	71	85
12	D2	184/204 (90%)	183 (100%)	1 (0%)	88	95
13	E1	182/234 (78%)	179 (98%)	3 (2%)	62	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
14	E2	226/229 (99%)	222 (98%)	4 (2%)	59 76
15	F1	189/210 (90%)	187 (99%)	2 (1%)	73 87
16	F2	154/170 (91%)	154 (100%)	0	100 100
17	G1	181/224 (81%)	180 (99%)	1 (1%)	86 94
18	G2	201/219 (92%)	200 (100%)	1 (0%)	88 95
19	H1	167/169 (99%)	167 (100%)	0	100 100
20	H2	165/176 (94%)	164 (99%)	1 (1%)	86 94
21	I1	180/182 (99%)	179 (99%)	1 (1%)	86 94
22	I2	176/181 (97%)	170 (97%)	6 (3%)	37 56
23	J1	141/150 (94%)	139 (99%)	2 (1%)	67 82
24	J2	160/168 (95%)	160 (100%)	0	100 100
25	K2	82/132 (62%)	81 (99%)	1 (1%)	71 85
26	L1	167/178 (94%)	165 (99%)	2 (1%)	71 85
27	L2	119/141 (84%)	116 (98%)	3 (2%)	47 67
28	M1	113/117 (97%)	113 (100%)	0	100 100
29	N1	171/172 (99%)	168 (98%)	3 (2%)	59 76
30	N2	129/130 (99%)	129 (100%)	0	100 100
31	O1	175/176 (99%)	175 (100%)	0	100 100
32	O2	98/119 (82%)	96 (98%)	2 (2%)	55 74
33	P1	134/165 (81%)	133 (99%)	1 (1%)	84 92
34	P2	105/130 (81%)	104 (99%)	1 (1%)	76 88
35	Q1	158/160 (99%)	156 (99%)	2 (1%)	69 84
36	Q2	108/119 (91%)	105 (97%)	3 (3%)	43 63
37	R1	145/173 (84%)	144 (99%)	1 (1%)	84 92
38	R2	119/121 (98%)	118 (99%)	1 (1%)	81 91
39	S1	155/155 (100%)	154 (99%)	1 (1%)	86 94
40	S2	118/132 (89%)	117 (99%)	1 (1%)	81 91
41	T1	138/140 (99%)	137 (99%)	1 (1%)	84 92
42	T2	110/117 (94%)	109 (99%)	1 (1%)	78 90
43	U1	87/127 (68%)	85 (98%)	2 (2%)	50 70
44	U2	87/105 (83%)	87 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	V1	101/108 (94%)	101 (100%)	0	100	100
46	V2	65/65 (100%)	64 (98%)	1 (2%)	65	80
47	W1	52/129 (40%)	52 (100%)	0	100	100
48	W2	112/113 (99%)	111 (99%)	1 (1%)	78	90
49	X1	105/134 (78%)	105 (100%)	0	100	100
50	X2	111/115 (96%)	110 (99%)	1 (1%)	78	90
51	Y1	115/136 (85%)	113 (98%)	2 (2%)	60	78
52	Y2	108/116 (93%)	107 (99%)	1 (1%)	78	90
53	Z1	115/116 (99%)	114 (99%)	1 (1%)	78	90
54	Z2	57/105 (54%)	57 (100%)	0	100	100
55	a1	121/122 (99%)	119 (98%)	2 (2%)	60	78
56	a2	86/99 (87%)	85 (99%)	1 (1%)	71	85
57	b1	45/56 (80%)	44 (98%)	1 (2%)	52	71
58	b2	73/76 (96%)	73 (100%)	0	100	100
59	c1	78/98 (80%)	76 (97%)	2 (3%)	46	66
60	c2	53/61 (87%)	52 (98%)	1 (2%)	57	75
61	d1	98/110 (89%)	97 (99%)	1 (1%)	76	88
62	d2	48/49 (98%)	48 (100%)	0	100	100
63	e1	113/121 (93%)	113 (100%)	0	100	100
64	e2	41/112 (37%)	40 (98%)	1 (2%)	49	68
65	f1	86/88 (98%)	86 (100%)	0	100	100
66	g1	91/102 (89%)	90 (99%)	1 (1%)	73	87
67	g2	263/274 (96%)	260 (99%)	3 (1%)	73	87
68	h1	108/110 (98%)	106 (98%)	2 (2%)	57	75
69	i1	83/88 (94%)	82 (99%)	1 (1%)	71	85
70	j1	73/80 (91%)	73 (100%)	0	100	100
71	k1	64/65 (98%)	63 (98%)	1 (2%)	62	79
72	l1	45/46 (98%)	45 (100%)	0	100	100
73	m1	46/116 (40%)	45 (98%)	1 (2%)	52	71
74	n1	23/24 (96%)	23 (100%)	0	100	100
75	o1	91/95 (96%)	90 (99%)	1 (1%)	73	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
76	p1	74/75 (99%)	74 (100%)	0	100 100
77	r1	102/120 (85%)	101 (99%)	1 (1%)	76 88
All	All	9292/10465 (89%)	9199 (99%)	93 (1%)	77 88

5 of 93 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	Q2	141	TYR
52	Y2	14	THR
38	R2	119	VAL
43	U1	124	TYR
56	a2	39	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 124 such sidechains are listed below:

Mol	Chain	Res	Type
25	K2	77	GLN
62	d2	4	GLN
34	P2	32	GLN
61	d1	98	ASN
73	m1	84	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	22	1483/1939 (76%)	290 (19%)	10 (0%)
2	51	3236/4269 (75%)	570 (17%)	37 (1%)
3	71	119/120 (99%)	6 (5%)	0
4	81	147/158 (93%)	19 (12%)	0
All	All	4985/6486 (76%)	885 (17%)	47 (0%)

5 of 885 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	22	3	C
1	22	4	C
1	22	33	G
1	22	41	G
1	22	46	A

5 of 47 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	51	1052	G
2	51	1977	A
2	51	1079	U
2	51	1651	C
2	51	2858	C

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 210 ligands modelled in this entry, 210 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

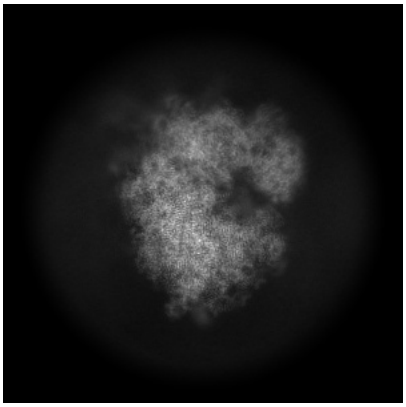
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13112. These allow visual inspection of the internal detail of the map and identification of artifacts.

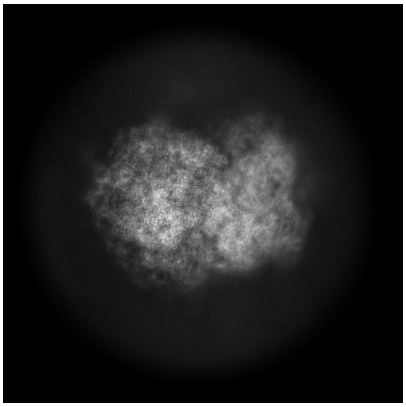
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

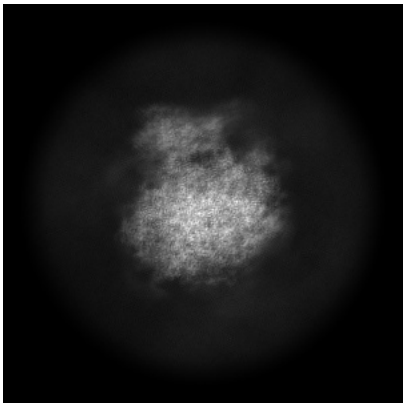
6.1.1 Primary map



X



Y

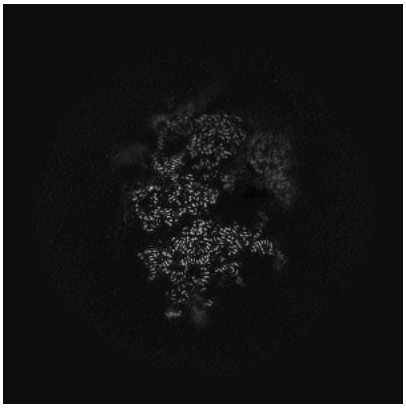


Z

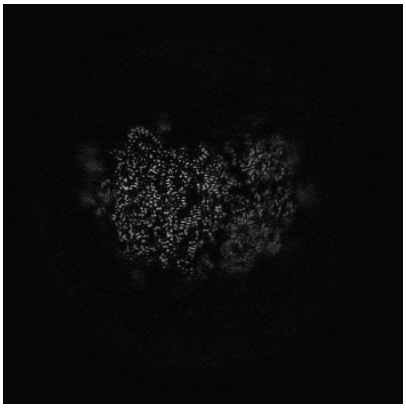
The images above show the map projected in three orthogonal directions.

6.2 Central slices

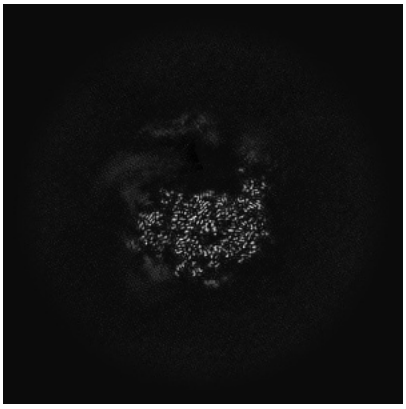
6.2.1 Primary map



X Index: 240



Y Index: 240

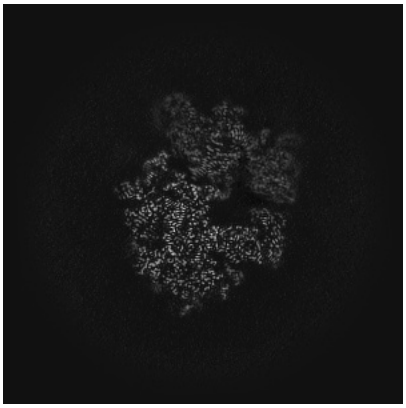


Z Index: 240

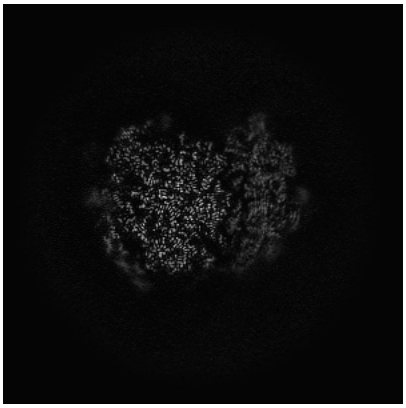
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

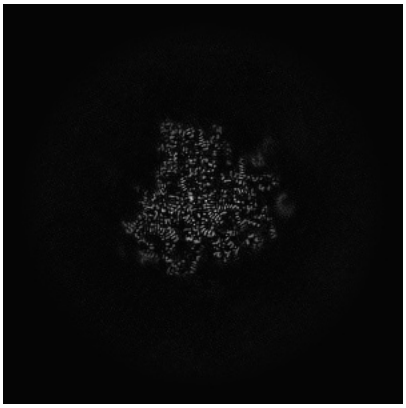
6.3.1 Primary map



X Index: 221



Y Index: 228



Z Index: 195

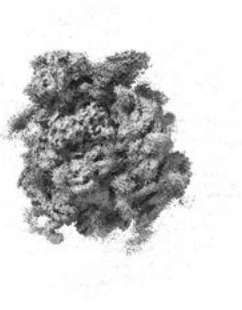
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

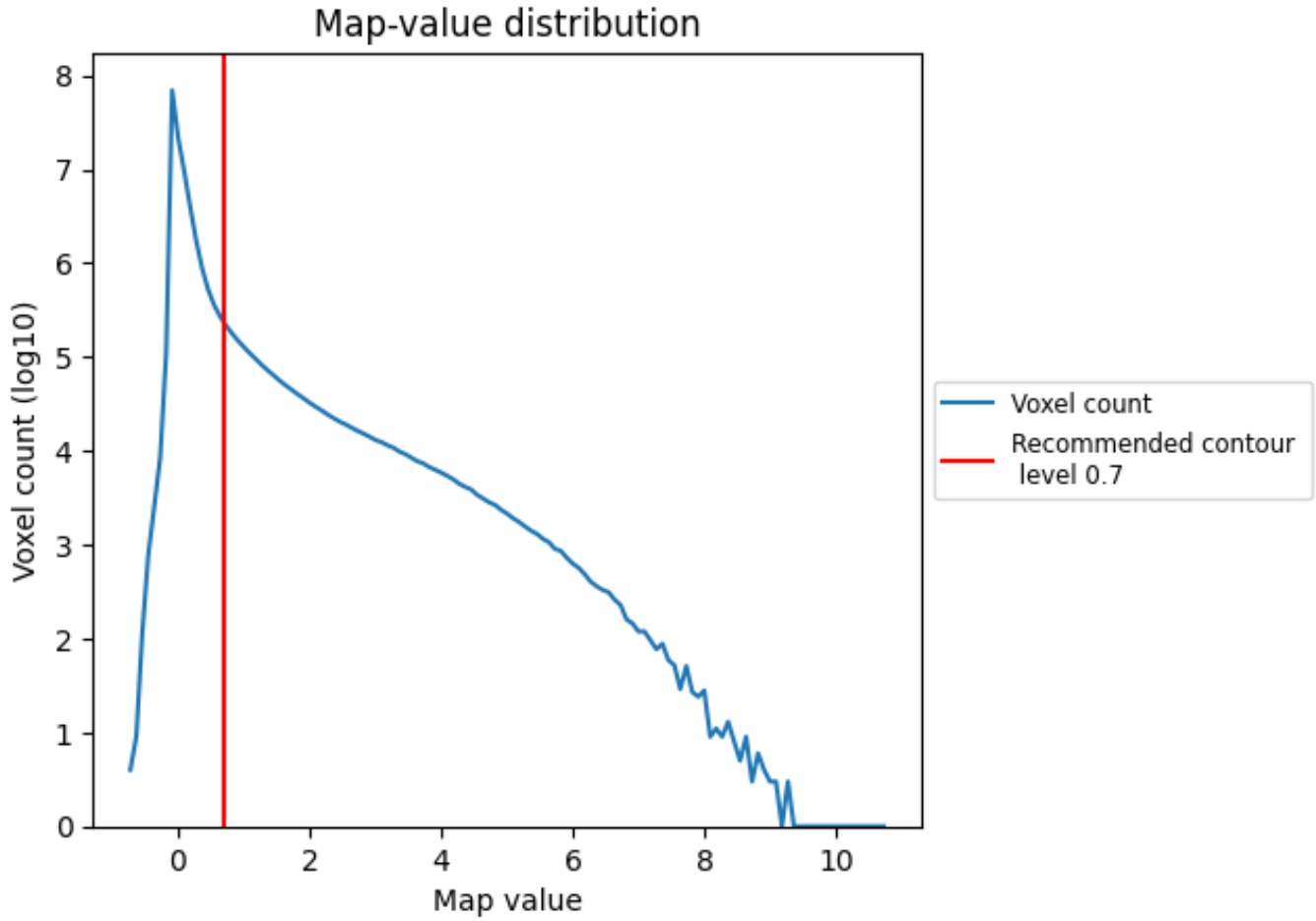
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

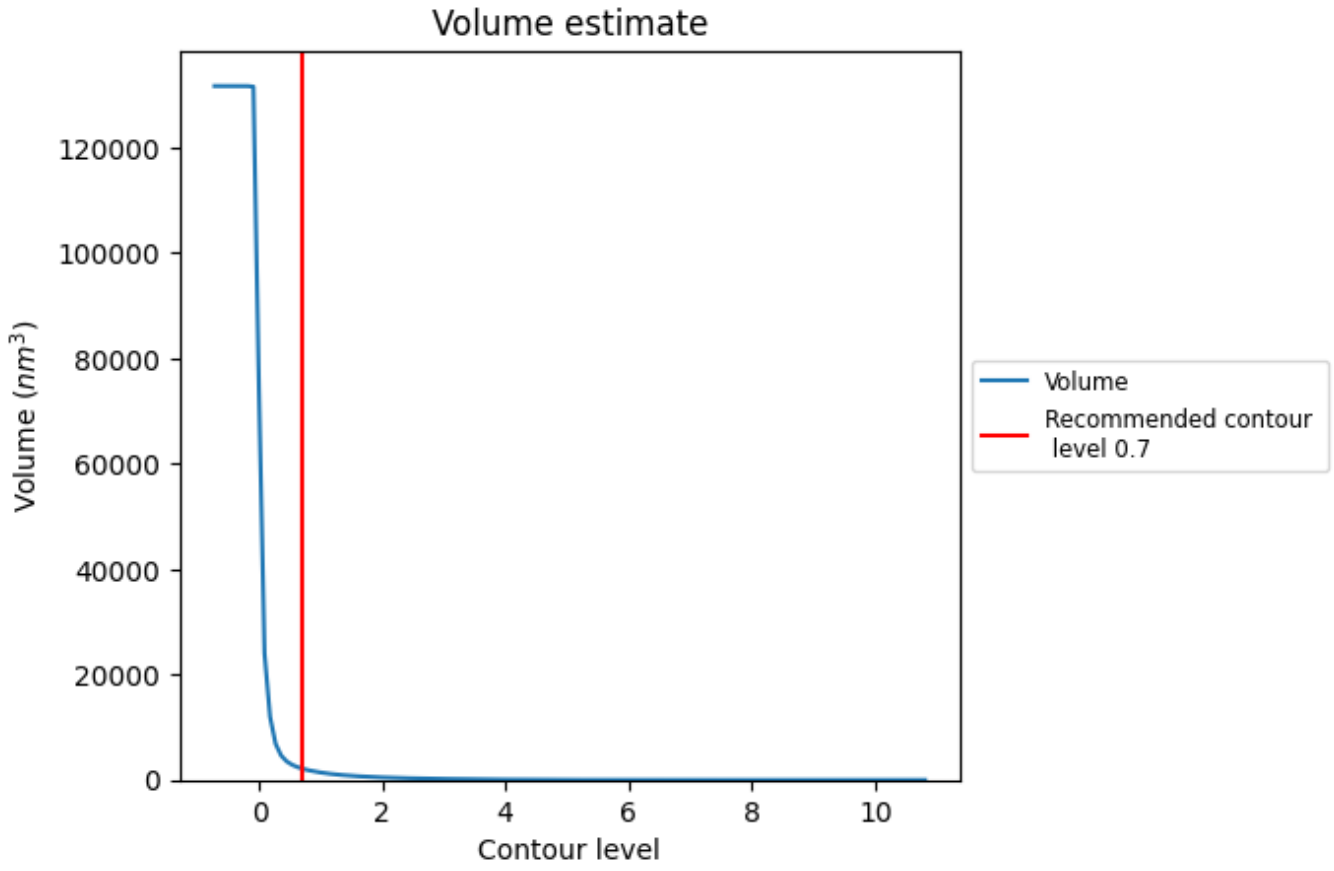
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

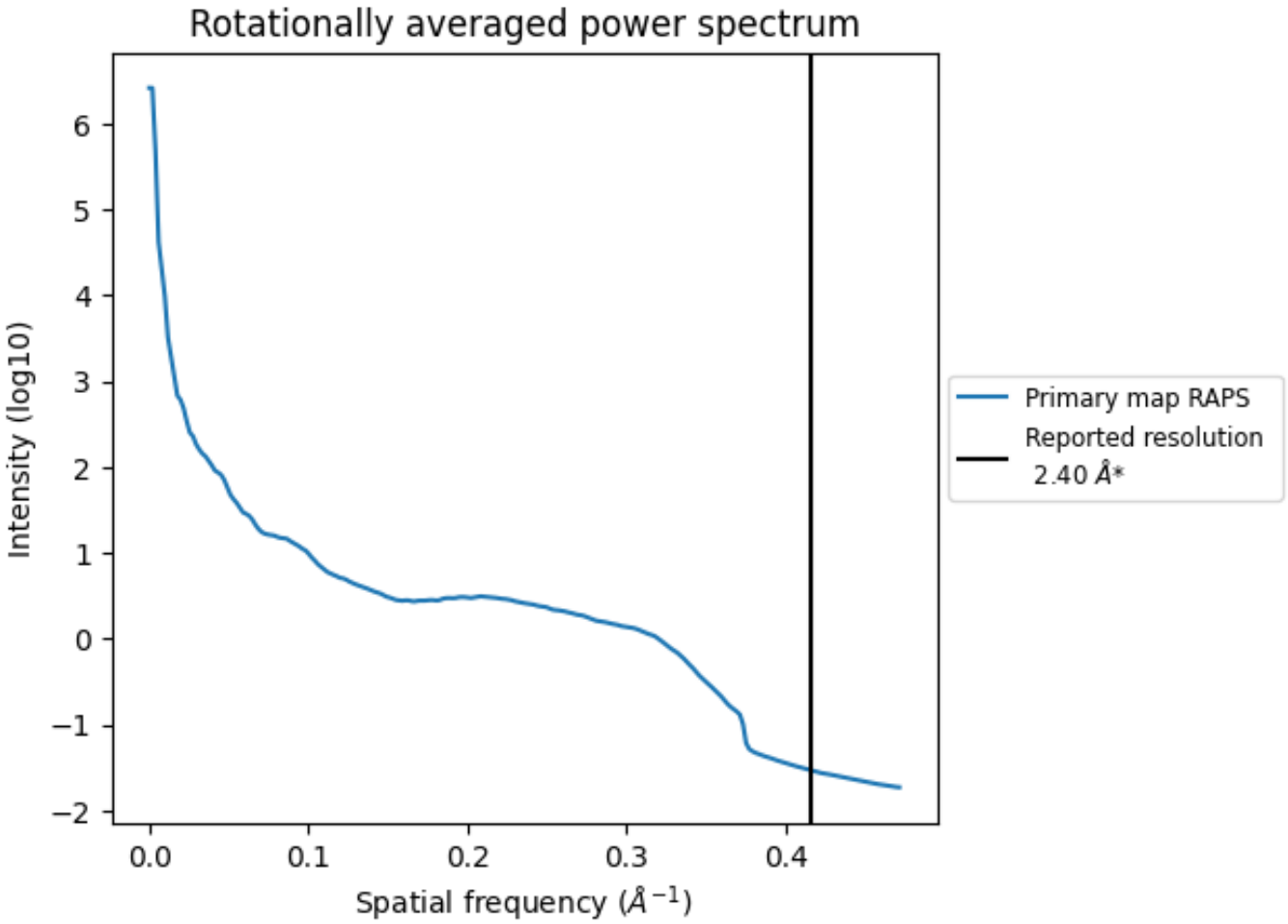
7.2 Volume estimate



The volume at the recommended contour level is 2168 nm^3; this corresponds to an approximate mass of 1959 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.417 Å^{-1}

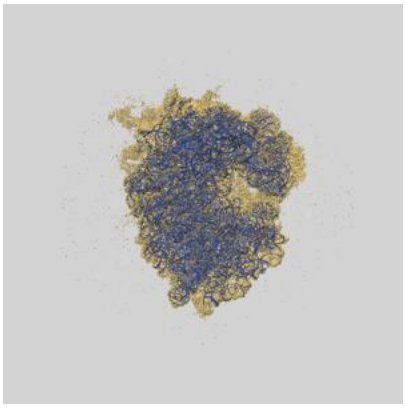
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

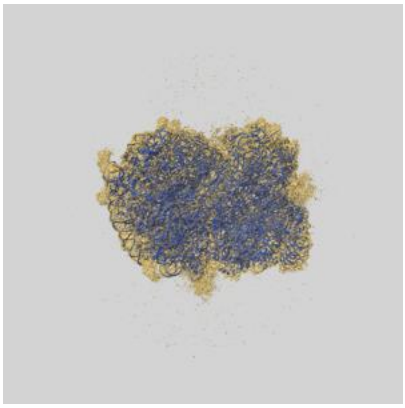
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-13112 and PDB model 7OYB. Per-residue inclusion information can be found in section 3 on page 18.

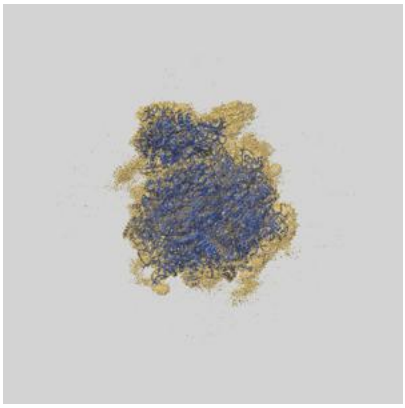
9.1 Map-model overlay



X



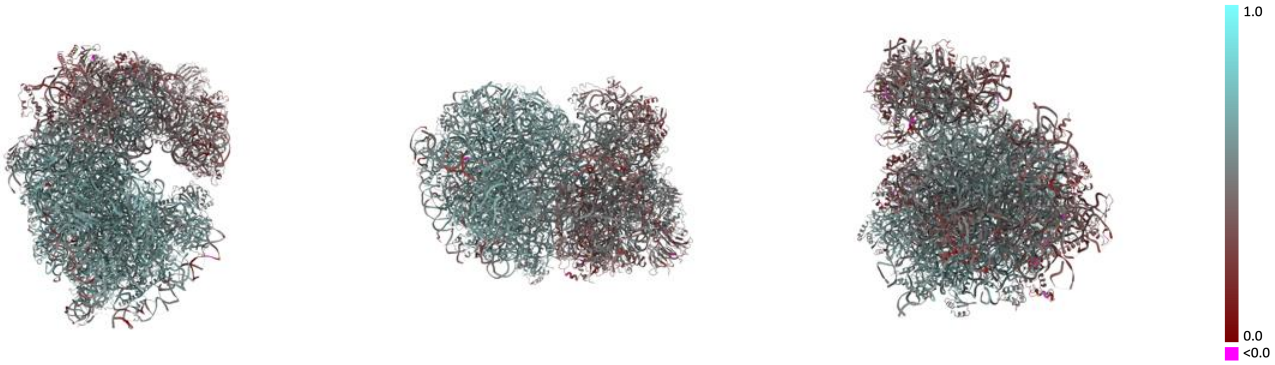
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

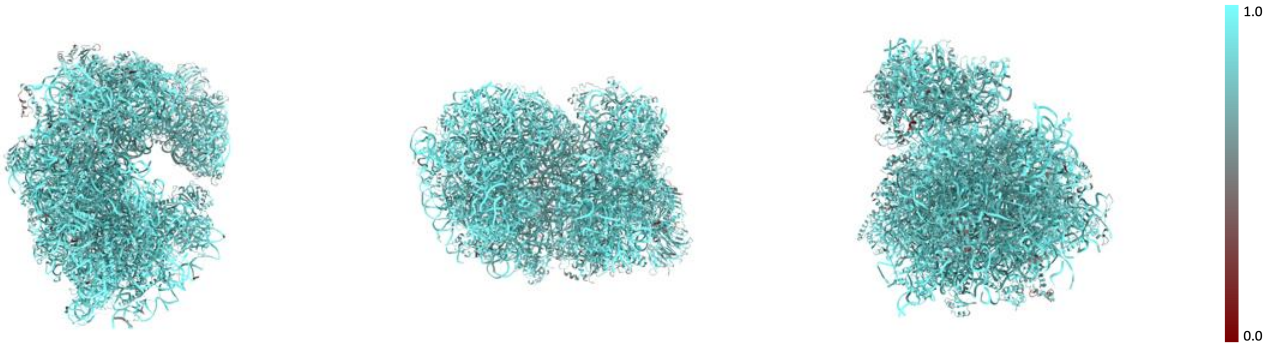
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

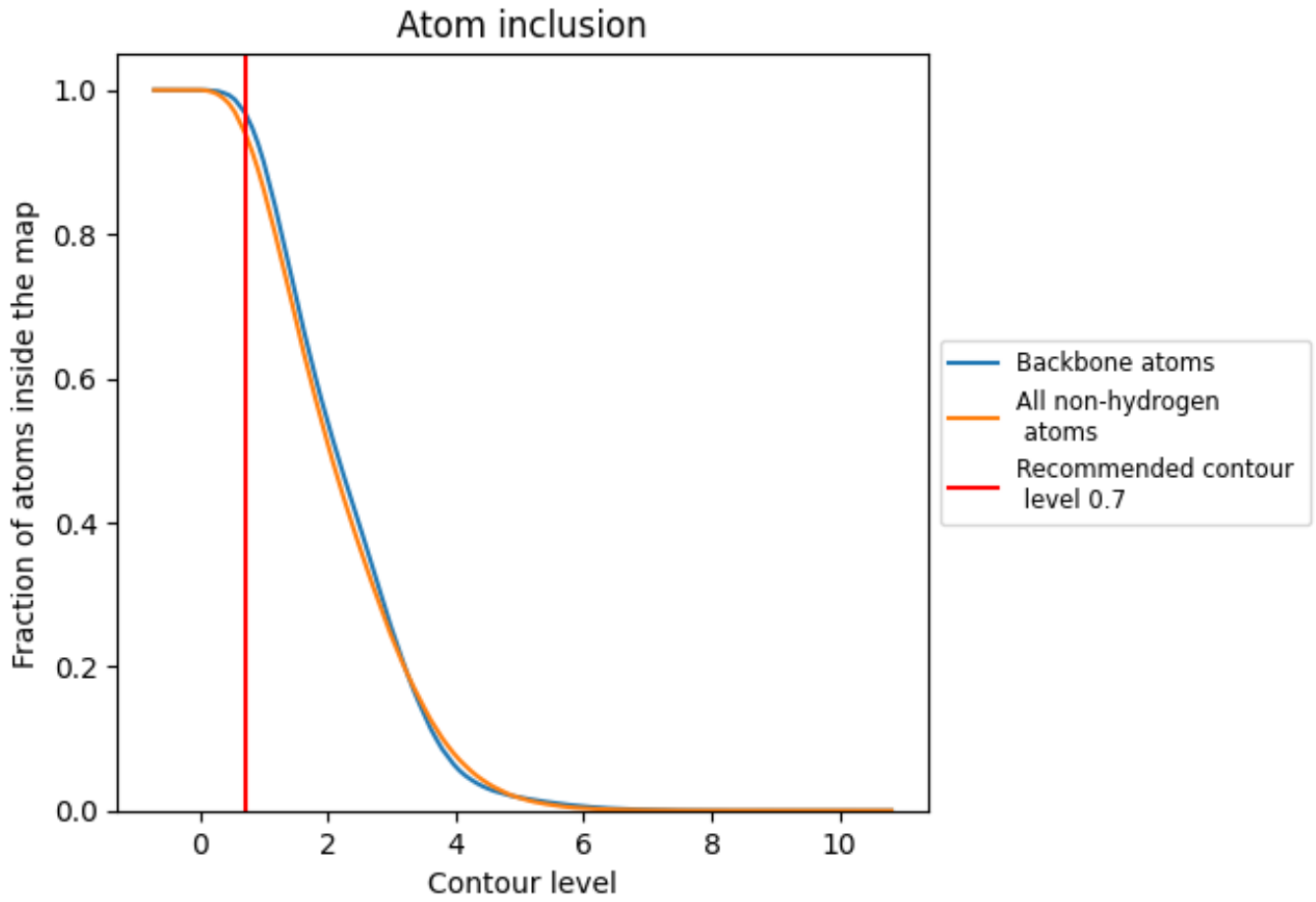
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.7).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9407	0.5280
22	0.9610	0.4440
51	0.9772	0.5840
71	0.9984	0.6170
81	0.9853	0.5990
A1	0.9715	0.6120
A2	0.9084	0.4950
B1	0.9636	0.6140
B2	0.7725	0.3260
C1	0.9642	0.6040
C2	0.9190	0.5240
D1	0.9388	0.5730
D2	0.8186	0.3590
E1	0.9380	0.5720
E2	0.8425	0.3590
F1	0.9618	0.6130
F2	0.7953	0.3820
G1	0.9032	0.5450
G2	0.7823	0.3760
H1	0.9415	0.5930
H2	0.7594	0.3530
I1	0.9107	0.5850
I2	0.7897	0.3790
J1	0.8789	0.5300
J2	0.8976	0.4040
K2	0.8677	0.3160
L1	0.9025	0.5750
L2	0.8114	0.3640
M1	0.9596	0.6040
N1	0.9795	0.6220
N2	0.8263	0.3430
O1	0.9677	0.6150
O2	0.8221	0.3390
P1	0.9667	0.6160
P2	0.8698	0.3940

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Chain	Atom inclusion	Q-score
Q1	0.9728	0.6120
Q2	0.8707	0.4080
R1	0.9386	0.5540
R2	0.7601	0.3950
S1	0.9730	0.6220
S2	0.8097	0.3730
T1	0.9423	0.6060
T2	0.8991	0.4280
U1	0.8656	0.4930
U2	0.8318	0.3990
V1	0.9536	0.5990
V2	0.8797	0.5180
W1	0.9628	0.5890
W2	0.9257	0.5050
X1	0.9325	0.5930
X2	0.8828	0.4930
Y1	0.9422	0.5890
Y2	0.7760	0.3070
Z1	0.9552	0.5570
Z2	0.7767	0.3320
a1	0.9691	0.6070
a2	0.8979	0.4490
b1	0.9433	0.5940
b2	0.8355	0.3450
c1	0.9703	0.5630
c2	0.7734	0.3430
d1	0.9321	0.5840
d2	0.9365	0.4270
e1	0.9729	0.6190
e2	0.7786	0.3640
f1	0.9759	0.6320
g1	0.9699	0.5990
g2	0.8046	0.3800
h1	0.9229	0.5820
i1	0.9259	0.5740
j1	0.9746	0.6200
k1	0.8438	0.5270
l1	0.9249	0.5740
m1	0.9651	0.6110
n1	0.8714	0.5300
o1	0.9373	0.5960
p1	0.9375	0.5820

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Chain	Atom inclusion	Q-score
r1	0.9637	0.5940